

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Maertens, Geert
Bosman, Fons
De Martynoff, Guy
Buyse, Marie-Ange

(ii) TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and therapeutic use.

(iii) NUMBER OF SEQUENCES: 122

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: NIXON & VANDERHYE
(B) STREET: 1100 North Glebe Road, 8th Floor
(C) CITY: Arlington, VA 22201
(E) COUNTRY: USA
(F) ZIP: 22201

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DCS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: Unassigned
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Sadoff, B. J.
(B) REGISTRATION NUMBER: 36663
(C) REFERENCE/DOCKET NUMBER: 2551-61

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (703) 816-4000
(B) TELEFAX: (703) 816-4100

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

*All
Cancelled*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCATGCAAG CTTAATTAAT T

21

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CCGGGGAGGC CTGCACGTGA TCGAGGGCAG ACACCATCAC CACCATCACT AATAGTTAAT
TAACTGCA

60

68

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 642 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..639

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTA CTG TCC TGT
Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys
1 5 10 15

48

CTG ACC ATT CCA GCT TCC GCT TAT GAG GTG CGC AAC GTG TCC GGG ATG
Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Met
20 25 30

96

TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG TAT GAG GCA
Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala

144

35	40	45	
GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu 50 55 60			192
AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG CTC GCA GCT Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala 65 70 75 80			240
AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC GTC GAT TTG Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu 85 90 95			288
CTC GTT GGG GCG GCT GCT CTC TGT TCC GCT ATG TAC GTG GGG GAT CTC Leu Val Gly Ala Ala Ala Leu Cys Ser Ala Met Tyr Val Gly Asp Leu 100 105 110			336
TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC TCG CCT CGC Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile Ser Pro Arg 115 120 125			384
CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His 130 135 140			432
ATA ACA GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro 145 150 155 160			480
ACA ACG GCC CTG GTG GTA TCG CAG CTG CTC CGG ATC CCA CAA GCT GTC Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val 165 170 175			528
GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG GGC CTC GCC Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala 180 185 190			576
TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT GTG ATG CTA Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu 195 200 205			624
CTC TTT GCT CTC TAATAG Leu Phe Ala Leu 210			642

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys
1				5					10					15	
Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Met

20										25										30																																		
Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala																																							
		35					40					45																																										
Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu																																							
		50				55					60																																											
Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala																																							
		65			70					75																																												
Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu																																							
				85					90																																													
Leu	Val	Gly	Ala	Ala	Ala	Leu	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu																																							
			100					105																																														
Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg																																							
		115					120					125																																										
Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His																																							
						135					140																																											
Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	Ser	Pro																																							
					150				155																																													
Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro	Gln	Ala	Val																																							
				165					170																																													
Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	Ala	Gly	Leu	Ala																																							
			180					185																																														
Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Ile	Val	Met	Leu																																							
		195					200																																															
Leu	Phe	Ala	Leu																																																			
		210																																																				

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 795 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..792

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATG	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTT	ACA	TGC	GGC	TTC	GCC	GAC	CTC	48
Met	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu	
1				5					10					15		
GTG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCC	CTA	GGG	GGC	GCT	GCC	AGG	96
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	
			20					25					30			
GCC	CTG	GCG	CAT	GGC	GTC	CGG	GTT	CTG	GAG	GAC	GGC	GTG	AAC	TAT	GCA	144
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	
		35					40					45				
ACA	GGG	AAT	TTG	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	TTG	GCT	TTG	192
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	
	50					55					60					
CTG	TCC	TGT	CTG	ACC	GTT	CCA	GCT	TCC	GCT	TAT	GAA	GTG	CGC	AAC	GTG	240
Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	
65					70					75				80		
TCC	GGG	ATG	TAC	CAT	GTC	ACG	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATT	GTG	288
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	
				85					90					95		
TAT	GAG	GCA	GCG	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	336
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	
			100					105					110			
GTT	CGG	GAG	AAC	AAC	TCT	TCC	CGC	TGC	TGG	GTA	GCG	CTC	ACC	CCC	ACG	384
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	
		115					120					125				
CTC	GCA	GCT	AGG	AAC	GCC	AGC	GTC	CCC	ACC	ACG	ACA	ATA	CGA	CGC	CAC	432
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	
		130					135					140				
GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	GCT	TTC	TGT	TCC	GCT	ATG	TAC	GTG	480
Val	Asp	Leu	Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	
145					150					155				160		
GGG	GAC	CTC	TGC	GGA	TCT	GTC	TTC	CTC	GTC	TCC	CAG	CTG	TTC	ACC	ATC	528
Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile	
				165					170					175		
TCG	CCT	CGC	CGG	CAT	GAG	ACG	GTG	CAG	GAC	TGC	AAT	TGC	TCA	ATC	TAT	576
Ser	Pro	Arg	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	
			180					185					190			
CCC	GGC	CAC	ATA	ACG	GGT	CAC	CGT	ATG	GCT	TGG	GAT	ATG	ATG	ATG	AAC	624
Pro	Gly	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	
		195					200					205				
TGG	TCG	CCT	ACA	ACG	GCC	CTG	GTG	GTA	TCG	CAG	CTG	CTC	CGG	ATC	CCA	672
Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro	
		210					215					220				
CAA	GCT	GTC	GTG	GAC	ATG	GTG	GCG	GGG	GCC	CAT	TGG	GGA	GTC	CTG	GCG	720
Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	Ala	
225					230					235				240		
GGT	CTC	GCC	TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	TTG	ATT	768

Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile
 245 250 255

GTG ATG CTA CTC TTT GCT CCC TAATAG
 Val Met Leu Leu Phe Ala Pro
 260

795

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu
 1 5 10 15

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg
 20 25 30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala
 35 40 45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu
 50 55 60

Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val
 65 70 75 80

Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val
 85 90 95

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys
 100 105 110

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
 115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His
 130 135 140

Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val
 145 150 155 160

Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile
 165 170 175

Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr
 180 185 190

Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn
 195 200 205

Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 210 215 220

Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala

(2) INFORMATION FOR SEQ ID NO: 7:

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..630

(ix) FEATURE:

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(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..627
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATG	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTT	ACG	TGC	GGC	TTC	GCC	GAC	CTC	48
Met	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu	
1				5					10					15		
ATG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCC	CTA	GGG	GGT	GCT	GCC	AGA	96
Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	
			20					25					30			
GCC	CTG	GCG	CAT	GGC	GTC	CGG	GTT	CTG	GAA	GAC	GGC	GTG	AAC	TAT	GCA	144
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	
			35				40					45				
ACA	GGG	AAT	TTG	CCT	GGT	TGC	TCT	TTC	TCT	ATC	FTC	CTC	TTG	GCT	TTA	192
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	
	50					55					60					
CTG	TCC	TGT	CTG	ACC	ATT	CCA	GCT	TCC	GCT	TAT	GAG	GTG	CGC	AAC	GTG	240
Leu	Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	
65					70				75					80		
TCC	GGG	ATG	TAC	CAT	GTC	ACG	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATT	GTG	288
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	
				85					90					95		
TAT	GAG	GCA	GCG	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	336
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	
			100					105					110			

GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACT ACG ACA ATA CGA CGC CAC	432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His	
130 135 140	
GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TGT TCC GCT ATG TAC GTG	480
Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val	
145 150 155 160	
GGG GAT CTC TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC	528
Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile	
165 170 175	
TCG CCT CGC CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT	576
Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr	
180 185 190	
CCC GGC CAC ATA ACA GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC	624
Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn	
195 200 205	
TGG TAATAG	633
Trp	
210	

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu
1				5					10					15	
Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg
			20					25					30		
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala
	35						40					45			
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu
	50					55					60				
Leu	Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val
	65				70					75				80	
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val
				85					90					95	
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys
			100					105					110		

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
 115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His
 130 135 140

Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val
 145 150 155 160

Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile
 165 170 175

Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr
 180 185 190

Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn
 195 200 205

Trp

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 483 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..480

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCC CTG CTG TCC TGT	48
Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys	
1 5 10 15	
CTG ACC ATA CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG TCC GGG GTG	96
Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val	
20 25 30	
TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATA GTG TAT GAG GCA	144
Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala	
35 40 45	
GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG	192
Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu	
50 55 60	

GGC AAC TCC TCC CGT TGC TGG GTG GCG CTC ACT CCC ACG CTC GCG GCC	240
Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala	
65 70 75 80	
AGG AAC GCC AGC GTC CCC ACA ACG ACA ATA CGA CGC CAC GTC GAT TTG	288
Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu	
85 90 95	
CTC GTT GGG GCT GCT GCT TTC TGT TCC GCT ATG TAC GTG GGG GAT CTC	336
Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu	
100 105 110	
TGC GGA TCT GTT TTC CTT GTT TCC CAG CTG TTC ACC TTC TCA CCT CGC	384
Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg	
115 120 125	
CGG CAT CAA ACA GTA CAG GAC TGC AAC TGC TCA ATC TAT CCC GGC CAT	432
Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His	
130 135 140	
GTA TCA GGT CAC CGC ATG GCT TGG GAT ATG ATG ATG AAC TGG TCC TAATAG	483
Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser	
145 150 155 160	

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 159 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys	
1 5 10 15	
Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val	
20 25 30	
Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala	
35 40 45	
Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu	
50 55 60	
Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala	
65 70 75 80	
Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu	
85 90 95	
Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu	
100 105 110	
Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg	
115 120 125	
Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His	

130

135

140

Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser
 145 150 155

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..477

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATG TCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCC CTG CTG TCC TGT	48
Met Ser Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys	
1 5 10 15	
CTG ACC ATA CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG TCC GGG GTG	96
Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val	
20 25 30	
TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATA GTG TAT GAG GCA	144
Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala	
35 40 45	
GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG	192
Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu	
50 55 60	
GGC AAC TCC TCC CGT TGC TGG GTG GCG CTC ACT CCC ACG CTC GCG GCC	240
Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala	
65 70 75 80	
AGG AAC GCC AGC GTC CCC ACA ACG ACA ATA CGA CGC CAC GTC GAT TTG	288
Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu	
85 90 95	
CTC GTT GGG GCT GCT GCT TTC TGT TCC GCT ATG TAC GTG GGG GAT CTC	336
Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu	
100 105 110	
TGC GGA TCT GTT TTC CTT GTT TCC CAG CTG TTC ACC TTC TCA CCT CGC	384
Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg	

115	120	125	
CGG CAT CAA ACA GTA CAG GAC	TGC AAC TGC TCA ATC TAT CCC GGC CAT		432
Arg His Gln Thr Val Gln Asp	Cys Asn Cys Ser Ile Tyr Pro Gly His		
130	135	140	
GTA TCA GGT CAC CGC ATG GCT TGG GAT ATG ATG ATG AAC TGG TAATAG			480
Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp			
145	150	155	

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met	Ser	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys
1				5					10					15	
Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val
			20					25					30		
Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala
		35				40						45			
Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu
	50					55					60				
Gly	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala
	65				70					75				80	
Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu
				85					90					95	
Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu
			100					105					110		
Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg
			115				120					125			
Arg	His	Gln	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His
	130					135					140				
Val	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp		
145					150				155						

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..633

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 1..630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATG	CTG	GGT	AAG	GCC	ATC	GAT	ACC	CTT	ACG	TGC	GGC	TTC	GCC	GAC	CTC	48
Met	Leu	Gly	Lys	Ala	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu	
1				5					10					15		
GTG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCC	CTA	GGG	GGC	GCT	GCC	AGG	96
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	
			20					25					30			
GCC	CTG	GCG	CAT	GGC	GTC	CGG	GTT	CTG	GAA	GAC	GGC	GTG	AAC	TAT	GCA	144
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	
		35					40					45				
ACA	GGG	AAT	TTG	CCT	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	TTG	GCT	TTA	192
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	
	50					55					60					
CTG	TCC	TGT	CTA	ACC	ATT	CCA	GCT	TCC	GCT	TAC	GAG	GTG	CGC	AAC	GTG	240
Leu	Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	
65					70					75					80	
TCC	GGG	ATG	TAC	CAT	GTC	ACG	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATT	GTG	288
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	
				85					90					95		
TAT	GAG	GCA	GCG	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	336
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	
			100					105					110			
GTT	CGG	GAG	AAC	AAC	TCT	TCC	CGC	TGC	TGG	GTA	GCG	CTC	ACC	CCC	ACG	384
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	
		115					120					125				
CTC	GCG	GCT	AGG	AAC	GCC	AGC	ATC	CCC	ACT	ACA	ACA	ATA	CGA	CGC	CAC	432
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Ile	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	
		130				135						140				
GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	GCT	TTC	TGT	TCC	GCT	ATG	TAC	GTG	480
Val	Asp	Leu	Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	
145					150					155					160	
GGG	GAT	CTC	TGC	GGA	TCT	GTC	TTC	CTC	GTC	TCC	CAG	CTG	TTC	ACC	ATC	528
Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile	
				165					170					175		
TCG	CCT	CGC	CGG	CAT	GAG	ACG	GTG	CAG	GAC	TGC	AAT	TGC	TCA	ATC	TAT	576
Ser	Pro	Arg	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	

180	185	190	
CCC GGC CAC ATA ACG GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC			624
Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn			
195	200	205	
TGG TAC TAATAG			640
Trp Tyr			
210			

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met	Leu	Gly	Lys	Ala	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu
1				5					10					15	
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg
			20					25					30		
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala
		35					40					45			
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu
		50				55					60				
Leu	Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val
65					70					75					80
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val
				85					90					95	
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys
			100					105					110		
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr
			115				120					125			
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Ile	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His
		130				135					140				
Val	Asp	Leu	Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val
145					150					155					160
Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile
				165					170					175	
Ser	Pro	Arg	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr
			180					185					190		
Pro	Gly	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn
			195				200					205			

Trp Tyr
210

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ATGCCCGGTT GCTCTTCTC TATCTT

26

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ATGTTGGGTA AGGTCATCGA TACCCT

26

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CTATTAGGAC CAGTTCATCA TCATATCCCA

30

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CTATTACCAG TTCATCATCA TATCCCA

27

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ATACGACGCC ACGTCGATTC CCAGCTGTTC ACCATC

36

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GATGGTGAAC AGCTGGGAAT CGACGTGGCG TCGTAT

36

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 723 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..720

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	
TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC	336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC	432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His	
130 135 140	
GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG	480
Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val	

145		150		155		160	
CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT							528
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg							
		165		170		175	
ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG							576
Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val							
		180		185		190	
GTA TCG CAG CTG CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG							624
Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala							
		195		200		205	
GGG GCC CAT TGG GGA GTC CTG GCG GGT CTC GCC TAC TAT TCC ATG GTG							672
Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val							
		210		215		220	
GGG AAC TGG GCT AAG GTT TTG ATT GTG ATG CTA CTC TTT GCT CCC TAATAG							723
Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu Leu Phe Ala Pro							
		225		230		235	240

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 239 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu
1				5					10					15	
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg
			20					25					30		
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala
			35				40						45		
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu
		50				55					60				
Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val
		65			70					75				80	
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val
				85					90					95	
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys
			100					105					110		
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr
			115				120					125			
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His
			130				135					140			
Val	Asp	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	Arg	His	Glu	Thr	Val

145		150		155		160
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg						
	165			170		175
Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val						
	180			185		190
Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala						
	195			200		205
Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val						
	210			215		220
Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu Leu Phe Ala Pro						
	225			230		235

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 561 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..558

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	

65	70	75	80	
TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG				288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	85	90	95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC				336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	100	105	110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG				384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	115	120	125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC				432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His	130	135	140	
GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG				480
Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val	145	150	155	160
CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT				528
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg	165	170	175	
ATG GCT TGG GAT ATG ATG ATG AAC TGG TAATAG				561
Met Ala Trp Asp Met Met Met Asn Trp	180	185		

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Met	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu
1				5					10					15	
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg
			20					25					30		
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala
		35					40					45			
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu
		50				55					60				
Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val
	65				70					75				80	
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val
				85					90					95	
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys
			100					105					110		

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
 115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His
 130 135 140

Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val
 145 150 155 160

Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg
 165 170 175

Met Ala Trp Asp Met Met Met Asn Trp
 180 185

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 606 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..603

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	

TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC	336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC	432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His	
130 135 140	
GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG	480
Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val	
145 150 155 160	
CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT	528
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg	
165 170 175	
ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG	576
Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val	
180 185 190	
GTA TCG CAG CTG CTC CGG ATC CTC TAATAG	606
Val Ser Gln Leu Leu Arg Ile Leu	
195 200	

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys
 100 105 110
 Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
 115 120 125
 Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His
 130 135 140
 Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val
 145 150 155 160
 Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg
 165 170 175
 Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val
 180 185 190
 Val Ser Gln Leu Leu Arg Ile Leu
 195 200

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 636 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..633

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192

Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu		
50						55					60						
CTG	TCC	TGT	CTG	ACC	GTT	CCA	GCT	TCC	GCT	TAT	GAA	GTG	CGC	AAC	GTG	240	
Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val		
65					70					75					80		
TCC	GGG	ATG	TAC	CAT	GTC	ACG	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATT	GTG	288	
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val		
				85					90					95			
TAT	GAG	GCA	GCG	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	336	
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys		
			100					105					110				
GTT	CGG	GAG	AAC	AAC	TCT	TCC	CGC	TGC	TGG	GTA	GCG	CTC	ACC	CCC	ACG	384	
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr		
		115					120					125					
CTC	GCA	GCT	AGG	AAC	GCC	AGC	GTC	CCC	ACC	ACG	ACA	ATA	CGA	CGC	CAC	432	
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His		
		130					135					140					
GTC	GAT	TCC	CAG	CTG	TTC	ACC	ATC	TCG	CCT	CGC	CGG	CAT	GAG	ACG	GTG	480	
Val	Asp	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	Arg	His	Glu	Thr	Val		
	145					150				155					160		
CAG	GAC	TGC	AAT	TGC	TCA	ATC	TAT	CCC	GGC	CAC	ATA	ACG	GGT	CAC	CGT	528	
Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	Ile	Thr	Gly	His	Arg		
				165					170					175			
ATG	GCT	TGG	GAT	ATG	ATG	ATG	AAC	TGG	TCG	CCT	ACA	ACG	GCC	CTG	GTG	576	
Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val		
			180					185					190				
GTA	TCG	CAG	CTG	CTC	CGG	ATC	GTG	ATC	GAG	GGC	AGA	CAC	CAT	CAC	CAC	624	
Val	Ser	Gln	Leu	Leu	Arg	Ile	Val	Ile	Glu	Gly	Arg	His	His	His	His		
		195					200					205					
CAT	CAC	TAATAG														636	
His	His																
		210															

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 210 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu		
1				5					10					15			
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg		
			20					25					30				
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala		

35					40					45					
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu
50					55					60					
Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val
65					70					75					80
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val
				85					90					95	
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys
			100					105					110		
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr
	115					120					125				
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His
130					135					140					
Val	Asp	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	Arg	His	Glu	Thr	Val
145				150					155					160	
Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	Ile	Thr	Gly	His	Arg
			165						170					175	
Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val
			180					185					190		
Val	Ser	Gln	Leu	Leu	Arg	Ile	Val	Ile	Glu	Gly	Arg	His	His	His	His
	195					200						205			
His	His														
210															

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..627

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

ATG GGT AAG GTC ATC GAT ACC CTT ACG TGC GGA TTC GCC GAT CTC ATG

Met	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	
1				5					10					15		
GGG	TAC	ATC	CCG	CTC	GTC	GGC	GCT	CCC	GTA	GGA	GGC	GTC	GCA	AGA	GCC	96
Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	
			20					25					30			
CTT	GCG	CAT	GGC	GTG	AGG	GCC	CTT	GAA	GAC	GGG	ATA	AAT	TTC	GCA	ACA	144
Leu	Ala	His	Gly	Val	Arg	Ala	Leu	Glu	Asp	Gly	Ile	Asn	Phe	Ala	Thr	
		35					40					45				
GGG	AAT	TTG	CCC	GGT	TGC	TCC	TTT	TCT	ATT	TTC	CTT	CTC	GCT	CTG	TTC	192
Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Phe	
	50					55					60					
TCT	TGC	TTA	ATT	CAT	CCA	GCA	GCT	AGT	CTA	GAG	TGG	CGG	AAT	ACG	TCT	240
Ser	Cys	Leu	Ile	His	Pro	Ala	Ala	Ser	Leu	Glu	Trp	Arg	Asn	Thr	Ser	
	65				70					75					80	
GGC	CTC	TAT	GTC	CTT	ACC	AAC	GAC	TGT	TCC	AAT	AGC	AGT	ATT	GTG	TAC	288
Gly	Leu	Tyr	Val	Leu	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	
			85						90					95		
GAG	GCC	GAT	GAC	GTT	ATT	CTG	CAC	ACA	CCC	GGC	TGC	ATA	CCT	TGT	GTC	336
Glu	Ala	Asp	Asp	Val	Ile	Leu	His	Thr	Pro	Gly	Cys	Ile	Pro	Cys	Val	
			100					105					110			
CAG	GAC	GGC	AAT	ACA	TCC	ACG	TGC	TGG	ACC	CCA	GTG	ACA	CCT	ACA	GTG	384
Gln	Asp	Gly	Asn	Thr	Ser	Thr	Cys	Trp	Thr	Pro	Val	Thr	Pro	Thr	Val	
		115					120					125				
GCA	GTC	AAG	TAC	GTC	GGA	GCA	ACC	ACC	GCT	TCG	ATA	CGC	AGT	CAT	GTG	432
Ala	Val	Lys	Tyr	Val	Gly	Ala	Thr	Thr	Ala	Ser	Ile	Arg	Ser	His	Val	
		130				135					140					
GAC	CTA	TTA	GTG	GGC	GCG	GCC	ACG	ATG	TGC	TCT	GCG	CTC	TAC	GTG	GGT	480
Asp	Leu	Leu	Val	Gly	Ala	Ala	Thr	Met	Cys	Ser	Ala	Leu	Tyr	Val	Gly	
	145				150					155					160	
GAC	ATG	TGT	GGG	GCT	GTC	TTC	CTC	GTG	GGA	CAA	GCC	TTC	ACG	TTC	AGA	528
Asp	Met	Cys	Gly	Ala	Val	Phe	Leu	Val	Gly	Gln	Ala	Phe	Thr	Phe	Arg	
			165						170					175		
CCT	CGT	CGC	CAT	CAA	ACG	GTC	CAG	ACC	TGT	AAC	TGC	TCG	CTG	TAC	CCA	576
Pro	Arg	Arg	His	Gln	Thr	Val	Gln	Thr	Cys	Asn	Cys	Ser	Leu	Tyr	Pro	
			180					185					190			
GGC	CAT	CTT	TCA	GGA	CAT	CGA	ATG	GCT	TGG	GAT	ATG	ATG	ATG	AAC	TGG	624
Gly	His	Leu	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
		195					200					205				
TAATAG																634

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 208 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met
 1 5 10 15
 Gly Tyr Ile Pro Leu Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala
 20 25 30
 Leu Ala His Gly Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr
 35 40 45
 Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe
 50 55 60
 Ser Cys Leu Ile His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser
 65 70 75 80
 Gly Leu Tyr Val Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr
 85 90 95
 Glu Ala Asp Asp Val Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val
 100 105 110
 Gln Asp Gly Asn Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val
 115 120 125
 Ala Val Lys Tyr Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val
 130 135 140
 Asp Leu Leu Val Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly
 145 150 155 160
 Asp Met Cys Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg
 165 170 175
 Pro Arg Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro
 180 185 190
 Gly His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 195 200 205

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..627

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATG GGT AAG GTC ATC GAT ACC CTA ACG TGC GGA TTC GCC GAT CTC ATG	48
Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met	
1 5 10 15	
GGG TAT ATC CCG CTC GTA GGC GGC CCC ATT GGG GGC GTC GCA AGG GCT	96
Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile Gly Gly Val Ala Arg Ala	
20 25 30	
CTC GCA CAC GGT GTG AGG GTC CTT GAG GAC GGG GTA AAC TAT GCA ACA	144
Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr	
35 40 45	
GGG AAT TTA CCC GGT TGC TCT TTC TCT ATC TTT ATT CTT GCT CTT CTC	192
Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu	
50 55 60	
TCG TGT CTG ACC GTT CCG GCC TCT GCA GTT CCC TAC CGA AAT GCC TCT	240
Ser Cys Leu Thr Val Pro Ala Ser Ala Val Pro Tyr Arg Asn Ala Ser	
65 70 75 80	
GGG ATT TAT CAT GTT ACC AAT GAT TGC CCA AAC TCT TCC ATA GTC TAT	288
Gly Ile Tyr His Val Thr Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr	
85 90 95	
GAG GCA GAT AAC CTG ATC CTA CAC GCA CCT GGT TGC GTG CCT TGT GTC	336
Glu Ala Asp Asn Leu Ile Leu His Ala Pro Gly Cys Val Pro Cys Val	
100 105 110	
ATG ACA GGT AAT GTG AGT AGA TGC TGG GTC CAA ATT ACC CCT ACA CTG	384
Met Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile Thr Pro Thr Leu	
115 120 125	
TCA GCC CCG AGC CTC GGA GCA GTC ACG GCT CCT CTT CGG AGA GCC GTT	432
Ser Ala Pro Ser Leu Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val	
130 135 140	
GAC TAC CTA GCG GGA GGG GCT GCC CTC TGC TCC GCG TTA TAC GTA GGA	480
Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly	
145 150 155 160	
GAC GCG TGT GGG GCA CTA TTC TTG GTA GGC CAA ATG TTC ACC TAT AGG	528
Asp Ala Cys Gly Ala Leu Phe Leu Val Gly Gln Met Phe Thr Tyr Arg	
165 170 175	
CCT CGC CAG CAC GCT ACG GTG CAG AAC TGC AAC TGT TCC ATT TAC AGT	576
Pro Arg Gln His Ala Thr Val Gln Asn Cys Asn Cys Ser Ile Tyr Ser	
180 185 190	
GGC CAT GTT ACC GGC CAC CGG ATG GCA TGG GAT ATG ATG ATG AAC TGG	624
Gly His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp	
195 200 205	

TAATAG

630

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Met	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	1	5	10	15
Gly	Tyr	Ile	Pro	Leu	Val	Gly	Gly	Pro	Ile	Gly	Gly	Val	Ala	Arg	Ala	20	25	30	
Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	35	40	45	
Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Ile	Leu	Ala	Leu	Leu	50	55	60	
Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Val	Pro	Tyr	Arg	Asn	Ala	Ser	65	70	75	80
Gly	Ile	Tyr	His	Val	Thr	Asn	Asp	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	85	90	95	
Glu	Ala	Asp	Asn	Leu	Ile	Leu	His	Ala	Pro	Gly	Cys	Val	Pro	Cys	Val	100	105	110	
Met	Thr	Gly	Asn	Val	Ser	Arg	Cys	Trp	Val	Gln	Ile	Thr	Pro	Thr	Leu	115	120	125	
Ser	Ala	Pro	Ser	Leu	Gly	Ala	Val	Thr	Ala	Pro	Leu	Arg	Arg	Ala	Val	130	135	140	
Asp	Tyr	Leu	Ala	Gly	Gly	Ala	Ala	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	145	150	155	160
Asp	Ala	Cys	Gly	Ala	Leu	Phe	Leu	Val	Gly	Gln	Met	Phe	Thr	Tyr	Arg	165	170	175	
Pro	Arg	Gln	His	Ala	Thr	Val	Gln	Asn	Cys	Asn	Cys	Ser	Ile	Tyr	Ser	180	185	190	
Gly	His	Val	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	195	200	205	

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:
TGGGATATGA TGATGAAC TG C

23

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:
CTATTATGGT GGTAAGCCAC AGAGCAGGAG

30

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1476 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1473

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..1470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

TGG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG GTA TCG

48

Trp 1	Asp	Met	Met	Met 5	Asn	Trp	Ser	Pro	Thr 10	Thr	Ala	Leu	Val	Val 15	Ser	
CAG	CTG	CTC	CGG	ATC	CCA	CAA	GCT	GTC	GTG	GAC	ATG	GTG	GCG	GGG	GCC	96
Gln	Leu	Leu	Arg 20	Ile	Pro	Gln	Ala	Val 25	Val	Asp	Met	Val	Ala	Gly	Ala	
CAT	TGG	GGA	GTC	CTG	GCG	GGC	CTC	GCC	TAC	TAT	TCC	ATG	GTG	GGG	AAC	144
His	Trp	Gly 35	Val	Leu	Ala	Gly	Leu 40	Ala	Tyr	Tyr	Ser	Met 45	Val	Gly	Asn	
TGG	GCT	AAG	GTT	TTG	GTT	GTG	ATG	CTA	CTC	TTT	GCC	GGC	GTC	GAC	GGG	192
Trp	Ala	Lys 50	Val	Leu	Val	Val 55	Met	Leu	Leu	Phe	Ala 60	Gly	Val	Asp	Gly	
CAT	ACC	CGC	GTG	TCA	GGA	GGG	GCA	GCA	GCC	TCC	GAT	ACC	AGG	GGC	CTT	240
His	Thr	Arg	Val	Ser	Gly 70	Gly	Ala	Ala	Ala	Ser 75	Asp	Thr	Arg	Gly	Leu 80	
GTG	TCC	CTC	TTT	AGC	CCC	GGG	TCG	GCT	CAG	AAA	ATC	CAG	CTC	GTA	AAC	288
Val	Ser	Leu	Phe	Ser 85	Pro	Gly	Ser	Ala	Gln 90	Lys	Ile	Gln	Leu	Val 95	Asn	
ACC	AAC	GGC	AGT	TGG	CAC	ATC	AAC	AGG	ACT	GCC	CTG	AAC	TGC	AAC	GAC	336
Thr	Asn	Gly	Ser 100	Trp	His	Ile	Asn	Arg 105	Thr	Ala	Leu	Asn	Cys 110	Asn	Asp	
TCC	CTC	CAA	ACA	GGG	TTC	TTT	GCC	GCA	CTA	TTC	TAC	AAA	CAC	AAA	TTC	384
Ser	Leu	Gln 115	Thr	Gly	Phe	Phe	Ala 120	Ala	Leu	Phe	Tyr	Lys 125	His	Lys	Phe	
AAC	TCG	TCT	GGA	TGC	CCA	GAG	CGC	TTG	GCC	AGC	TGT	CGC	TCC	ATC	GAC	432
Asn	Ser	Ser 130	Gly	Cys	Pro	Glu 135	Arg	Leu	Ala	Ser 140	Cys	Arg	Ser	Ile	Asp	
AAG	TTC	GCT	CAG	GGG	TGG	GGT	CCC	CTC	ACT	TAC	ACT	GAG	CCT	AAC	AGC	480
Lys	Phe	Ala	Gln	Gly 145	Trp	Gly 150	Pro	Leu	Thr	Tyr 155	Thr	Glu	Pro	Asn	Ser 160	
TCG	GAC	CAG	AGG	CCC	TAC	TGC	TGG	CAC	TAC	GCG	CCT	CGA	CCG	TGT	GGT	528
Ser	Asp	Gln	Arg 165	Pro	Tyr	Cys	Trp	His 170	Tyr	Ala	Pro	Arg	Pro	Cys 175	Gly	
ATT	GTA	CCC	GCG	TCT	CAG	GTG	TGC	GGT	CCA	GTG	TAT	TGC	TTC	ACC	CCG	576
Ile	Val	Pro 180	Ala	Ser	Gln	Val	Cys 185	Gly	Pro	Val	Tyr	Cys 190	Phe	Thr	Pro	
AGC	CCT	GTT	GTG	GTG	GGG	ACG	ACC	GAT	CGG	TTT	GGT	GTC	CCC	ACG	TAT	624
Ser	Pro	Val 195	Val	Val	Gly	Thr	Thr 200	Asp	Arg	Phe	Gly	Val 205	Pro	Thr	Tyr	
AAC	TGG	GGG	GCG	AAC	GAC	TCG	GAT	GTG	CTG	ATT	CTC	AAC	AAC	ACG	CGG	672
Asn	Trp	Gly 210	Ala	Asn	Asp	Ser 215	Asp	Val	Leu	Ile	Leu 220	Asn	Asn	Thr	Arg	
CCG	CCG	CGA	GGC	AAC	TGG	TTC	GGC	TGT	ACA	TGG	ATG	AAT	GGC	ACT	GGG	720
Pro	Pro	Arg 225	Gly	Asn 230	Trp	Phe	Gly	Cys	Thr	Trp 235	Met	Asn	Gly	Thr 240	Gly	
TTC	ACC	AAG	ACG	TGT	GGG	GGC	CCC	CCG	TGC	AAC	ATC	GGG	GGG	GCC	GGC	768
Phe	Thr	Lys	Thr 245	Cys	Gly	Gly	Pro	Pro 250	Cys	Asn	Ile	Gly	Gly	Ala 255	Gly	

AAC Asn	AAC Asn	ACC Thr	TTG Leu	ACC Thr	TGC Cys	CCC Pro	ACT Thr	GAC Asp	TGT Cys	TTT Phe	CGG Arg	AAG Lys	CAC His	CCC Pro	GAG Glu	816
			260					265					270			
GCC Ala	ACC Thr	TAC Tyr	GCC Ala	AGA Arg	TGC Cys	GGT Gly	TCT Ser	GGG Gly	CCC Pro	TGG Trp	CTG Leu	ACA Thr	CCT Pro	AGG Arg	TGT Cys	864
		275					280					285				
ATG Met	GTT Val	CAT His	TAC Tyr	CCA Pro	TAT Tyr	AGG Arg	CTC Leu	TGG Trp	CAC His	TAC Tyr	CCC Pro	TGC Cys	ACT Thr	GTC Val	AAC Asn	912
	290					295					300					
TTC Phe	ACC Thr	ATC Ile	TTC Phe	AAG Lys	GTT Val	AGG Arg	ATG Met	TAC Tyr	GTG Val	GGG Gly	GGC Val	GTG Glu	GAG His	CAC Arg	AGG Arg	960
305					310					315					320	
TTC Phe	GAA Glu	GCC Ala	GCA Ala	TGC Cys	AAT Asn	TGG Trp	ACT Thr	CGA Arg	GGA Gly	GAG Glu	CGT Arg	TGT Cys	GAC Asp	TTG Leu	GAG Glu	1008
				325					330					335		
GAC Asp	AGG Arg	GAT Asp	AGA Arg	TCA Ser	GAG Glu	CTT Leu	AGC Ser	CCG Pro	CTG Leu	CTG Leu	CTG Leu	TCT Ser	ACA Thr	ACA Thr	GAG Glu	1056
			340					345					350			
TGG Trp	CAG Gln	ATA Ile	CTG Leu	CCC Pro	TGT Cys	TCC Ser	TTC Phe	ACC Thr	ACC Thr	CTG Leu	CCG Pro	GCC Ala	CTA Leu	TCC Ser	ACC Thr	1104
		355					360					365				
GGC Gly	CTG Leu	ATC Ile	CAC His	CTC Leu	CAT His	CAG Gln	AAC Asn	ATC Ile	GTG Val	GAC Asp	GTG Val	CAA Gln	TAC Tyr	CTG Leu	TAC Tyr	1152
	370					375					380					
GGT Gly	GTA Val	GGG Gly	TCG Ser	GCG Ala	GTT Val	GTC Val	TCC Ser	CTT Leu	GTC Val	ATC Ile	AAA Lys	TGG Trp	GAG Glu	TAT Tyr	GTC Val	1200
385					390					395					400	
CTG Leu	TTG Leu	CTC Leu	TTC Phe	CTT Leu	CTC Leu	CTG Leu	GCA Ala	GAC Asp	GCG Ala	CGC Arg	ATC Ile	TGC Cys	GCC Ala	TGC Cys	TTA Leu	1248
				405					410				415			
TGG Trp	ATG Met	ATG Met	CTG Leu	CTG Leu	ATA Ile	GCT Ala	CAA Gln	GCT Ala	GAG Glu	GCC Ala	GCC Ala	TTA Leu	GAG Glu	AAC Asn	CTG Leu	1296
			420				425					430				
GTG Val	GTC Val	CTC Leu	AAT Asn	GCG Ala	GCG Ala	GCC Ala	GTG Val	GCC Ala	GGG Gly	GCG Ala	CAT His	GGC Gly	ACT Thr	CTT Leu	TCC Ser	1344
		435					440					445				
TTC Phe	CTT Leu	GTG Val	TTC Phe	TTC Phe	TGT Cys	GCT Ala	GCC Ala	TGG Trp	TAC Tyr	ATC Ile	AAG Lys	GGC Gly	AGG Arg	CTG Leu	GTC Val	1392
	450					455					460					
CCT Pro	GGT Gly	GCG Ala	GCA Ala	TAC Tyr	GCC Ala	TTC Phe	TAT Tyr	GGC Gly	GTG Val	TGG Trp	CCG Pro	CTG Leu	CTC Leu	CTG Leu	CTT Leu	1440
465					470				475						480	
CTG Leu	CTG Leu	GCC Ala	TTA Leu	CCA Pro	CCA Pro	CGA Arg	GCT Ala	TAT Tyr	GCC Ala	TAGTAA						1476
				485					490							

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```

Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val Val Ser
 1           5           10           15
Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala
      20           25           30
His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn
      35           40           45
Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly
      50           55           60
His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu
      65           70           75           80
Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn
      85           90           95
Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp
      100          105          110
Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe
      115          120          125
Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp
      130          135          140
Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser
      145          150          155          160
Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly
      165          170          175
Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro
      180          185          190
Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr
      195          200          205
Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg
      210          215          220
Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly
      225          230          235          240
Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly
      245          250          255
Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu
      260          265          270
Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys

```

[illegible]

(2) INFORMATION FOR SEQ ID NO: 37:

- ```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1021 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 2..1018

(ix) FEATURE:
 (A) NAME/KEY: mac_peptide
```

(B) LOCATION: 2..1015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| G ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA   | 46  |
| Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly     |     |
| 1 5 10 15                                                       |     |
| GTC CTG GCG GGC CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG | 94  |
| Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys |     |
| 20 25 30                                                        |     |
| GTT TTG GTT GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG CAT ACC CGC | 142 |
| Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg |     |
| 35 40 45                                                        |     |
| GTG TCA GGA GGG GCA GCA GCC TCC GAT ACC AGG GGC CTT GTG TCC CTC | 190 |
| Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu |     |
| 50 55 60                                                        |     |
| TTT AGC CCC GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC AAC GGC | 238 |
| Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly |     |
| 65 70 75                                                        |     |
| AGT TGG CAC ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC CTC CAA | 286 |
| Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln |     |
| 80 85 90 95                                                     |     |
| ACA GGG TTC TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC TCG TCT | 334 |
| Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser |     |
| 100 105 110                                                     |     |
| GGA TGC CCA GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG TTC GCT | 382 |
| Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala |     |
| 115 120 125                                                     |     |
| CAG GGG TGG GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG GAC CAG | 430 |
| Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln |     |
| 130 135 140                                                     |     |
| AGG CCC TAC TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT ATT GTA CCC | 478 |
| Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro |     |
| 145 150 155                                                     |     |
| GCG TCT CAG GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC CCT GTT | 526 |
| Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val |     |
| 160 165 170 175                                                 |     |
| GTG GTG GGG ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT AAC TGG GGG | 574 |
| Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly |     |
| 180 185 190                                                     |     |
| GCG AAC GAC TCG GAT GTG CTG ATT CTC AAC AAC ACG CGG CCG CCG CGA | 622 |
| Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg |     |
| 195 200 205                                                     |     |
| GGC AAC TGG TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC ACC AAG | 670 |
| Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys |     |
| 210 215 220                                                     |     |
| ACG TGT GGG GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC AAC ACC | 718 |
| Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr |     |

| 225                                                             | 230 | 235 |      |
|-----------------------------------------------------------------|-----|-----|------|
| TTG ACC TGC CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG GCC ACC TAC |     |     | 766  |
| Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr |     |     |      |
| 240                                                             | 245 | 250 | 255  |
| GCC AGA TGC GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG GTT CAT |     |     | 814  |
| Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His |     |     |      |
|                                                                 | 260 | 265 | 270  |
| TAC CCA TAT AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC ACC ATC |     |     | 862  |
| Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile |     |     |      |
|                                                                 | 275 | 280 | 285  |
| TTC AAG GTT AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC GAA GCC |     |     | 910  |
| Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala |     |     |      |
|                                                                 | 290 | 295 | 300  |
| GCA TGC AAT TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC AGG GAT |     |     | 958  |
| Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp |     |     |      |
|                                                                 | 305 | 310 | 315  |
| AGA TCA GAG CTT AGC CCG CTG CTG CTG TCT ACA ACA GAG TGG CAG AGT |     |     | 1006 |
| Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp Gln Ser |     |     |      |
|                                                                 | 320 | 325 | 330  |
| GGC AGA GCT TAATTA                                              |     |     | 1021 |
| Gly Arg Ala                                                     |     |     |      |

## (2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 338 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Pro | Gln | Ala | Val | Val | Asp | Met | Val | Ala | Gly | Ala | His | Trp | Gly | Val |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Leu | Ala | Gly | Leu | Ala | Tyr | Tyr | Ser | Met | Val | Gly | Asn | Trp | Ala | Lys | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Val | Val | Met | Leu | Leu | Phe | Ala | Gly | Val | Asp | Gly | His | Thr | Arg | Val |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Gly | Gly | Ala | Ala | Ala | Ser | Asp | Thr | Arg | Gly | Leu | Val | Ser | Leu | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Pro | Gly | Ser | Ala | Gln | Lys | Ile | Gln | Leu | Val | Asn | Thr | Asn | Gly | Ser |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Trp | His | Ile | Asn | Arg | Thr | Ala | Leu | Asn | Cys | Asn | Asp | Ser | Leu | Gln | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gly | Phe | Phe | Ala | Ala | Leu | Phe | Tyr | Lys | His | Lys | Phe | Asn | Ser | Ser | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln  
 115 120 125  
 Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg  
 130 135 140  
 Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala  
 145 150 155 160  
 Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val  
 165 170 175  
 Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala  
 180 185 190  
 Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly  
 195 200 205  
 Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr  
 210 215 220  
 Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu  
 225 230 235 240  
 Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala  
 245 250 255  
 Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr  
 260 265 270  
 Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe  
 275 280 285  
 Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala  
 290 295 300  
 Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg  
 305 310 315 320  
 Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp Gln Ser Gly  
 325 330 335  
 Arg Ala

## (2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1034 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 2..1032

## (ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 2..1029

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| G ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA   | 46  |
| Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly     |     |
| 1 5 10 15                                                       |     |
| GTC CTG GCG GGC CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG | 94  |
| Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys |     |
| 20 25 30                                                        |     |
| GTT TTG GTT GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG CAT ACC CGC | 142 |
| Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg |     |
| 35 40 45                                                        |     |
| GTG TCA GGA GGG GCA GCA GCC TCC GAT ACC AGG GGC CTT GTG TCC CTC | 190 |
| Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu |     |
| 50 55 60                                                        |     |
| TTT AGC CCC GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC AAC GGC | 238 |
| Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly |     |
| 65 70 75                                                        |     |
| AGT TGG CAC ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC CTC CAA | 286 |
| Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln |     |
| 80 85 90 95                                                     |     |
| ACA GGG TTC TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC TCG TCT | 334 |
| Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser |     |
| 100 105 110                                                     |     |
| GGA TGC CCA GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG TTC GCT | 382 |
| Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala |     |
| 115 120 125                                                     |     |
| CAG GGG TGG GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG GAC CAG | 430 |
| Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln |     |
| 130 135 140                                                     |     |
| AGG CCC TAC TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT ATT GTA CCC | 478 |
| Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro |     |
| 145 150 155                                                     |     |
| GCG TCT CAG GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC CCT GTT | 526 |
| Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val |     |
| 160 165 170 175                                                 |     |
| GTG GTG GGG ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT AAC TGG GGG | 574 |
| Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly |     |
| 180 185 190                                                     |     |
| GCG AAC GAC TCG GAT GTG CTG ATT CTC AAC AAC ACG GGG CCG CCG CGA | 622 |
| Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg |     |
| 195 200 205                                                     |     |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| GGC AAC TGG TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC ACC AAG<br>Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys<br>210 215 220     | 670  |
| ACG TGT GGG GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC AAC ACC<br>Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr<br>225 230 235     | 718  |
| TTG ACC TGC CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG GCC ACC TAC<br>Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr<br>240 245 250 255 | 766  |
| GCC AGA TGC GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG GTT CAT<br>Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His<br>260 265 270     | 814  |
| TAC CCA TAT AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC ACC ATC<br>Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile<br>275 280 285     | 862  |
| TTC AAG GTT AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC GAA GCC<br>Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala<br>290 295 300     | 910  |
| GCA TGC AAT TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC AGG GAT<br>Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp<br>305 310 315     | 958  |
| AGA TCA GAG CTT AGC CCG CTG CTG CTG TCT ACA ACA GGT GAT CGA GGG<br>Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Gly Asp Arg Gly<br>320 325 330 335 | 1006 |
| CAG ACA CCA TCA CCA CCA TCA CTA AT AG<br>Gln Thr Pro Ser Pro Pro Ser Leu<br>340                                                                       | 1034 |

## (2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 343 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

|                                                                                |
|--------------------------------------------------------------------------------|
| Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val<br>1 5 10 15   |
| Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val<br>20 25 30    |
| Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val<br>35 40 45    |
| Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe<br>50 55 60    |
| Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser<br>65 70 75 80 |

[illegible]

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 945 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO



(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..942

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 1..939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG GTG GGG AAC TGG GCT AAG GTT TTG GTT GTG ATG CTA CTC TTT GCC | 48  |
| Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala |     |
| 1 5 10 15                                                       |     |
| GGC GTC GAC GGG CAT ACC CGC GTG TCA GGA GGG GCA GCA GCC TCC GAT | 96  |
| Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp |     |
| 20 25 30                                                        |     |
| ACC AGG GGC CTT GTG TCC CTC TTT AGC CCC GGG TCG GCT CAG AAA ATC | 144 |
| Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile |     |
| 35 40 45                                                        |     |
| CAG CTC GTA AAC ACC AAC GGC AGT TGG CAC ATC AAC AGG ACT GCC CTG | 192 |
| Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu |     |
| 50 55 60                                                        |     |
| AAC TGC AAC GAC TCC CTC CAA ACA GGG TTC TTT GCC GCA CTA TTC TAC | 240 |
| Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr |     |
| 65 70 75 80                                                     |     |
| AAA CAC AAA TTC AAC TCG TCT GGA TGC CCA GAG CGC TTG GCC AGC TGT | 288 |
| Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys |     |
| 85 90 95                                                        |     |
| CGC TCC ATC GAC AAG TTC GCT CAG GGG TGG GGT CCC CTC ACT TAC ACT | 336 |
| Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr |     |
| 100 105 110                                                     |     |
| GAG CCT AAC AGC TCG GAC CAG AGG CCC TAC TGC TGG CAC TAC GCG CCT | 384 |
| Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro |     |
| 115 120 125                                                     |     |
| CGA CCG TGT GGT ATT GTA CCC GCG TCT CAG GTG TGC GGT CCA GTG TAT | 432 |
| Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr |     |
| 130 135 140                                                     |     |
| TGC TTC ACC CCG AGC CCT GTT GTG GTG GGG ACG ACC GAT CGG TTT GGT | 480 |
| Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly |     |
| 145 150 155 160                                                 |     |
| GTC CCC ACG TAT AAC TGG GGG GCG AAC GAC TCG GAT GTG CTG ATT CTC | 528 |
| Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu |     |
| 165 170 175                                                     |     |
| AAC AAC ACG CGG CCG CCG CGA GGC AAC TGG TTC GGC TGT ACA TGG ATG | 576 |
| Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met |     |
| 180 185 190                                                     |     |

|                                                                                                                                                       |     |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| AAT GGC ACT GGG TTC ACC AAG ACG TGT GGG GGC CCC CCG TGC AAC ATC<br>Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile<br>195 200 205     | 624 |
| GGG GGG GCC GGC AAC AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT CGG<br>Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg<br>210 215 220     | 672 |
| AAG CAC CCC GAG GCC ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG CTG<br>Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu<br>225 230 235 240 | 720 |
| ACA CCT AGG TGT ATG GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC CCC<br>Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro<br>245 250 255     | 768 |
| TGC ACT GTC AAC TTC ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG GGC<br>Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly<br>260 265 270     | 816 |
| GTG GAG CAC AGG TTC GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG CGT<br>Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg<br>275 280 285     | 864 |
| TGT GAC TTG GAG GAC AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG CTG<br>Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu<br>290 295 300     | 912 |
| TCT ACA ACA GAG TGG CAG AGC TTA ATT AAT TAG<br>Ser Thr Thr Glu Trp Gln Ser Leu Ile Asn<br>305 310                                                     | 945 |

## (2) INFORMATION FOR SEQ ID NO: 42:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

|                                                                                |
|--------------------------------------------------------------------------------|
| Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala<br>1 5 10 15   |
| Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp<br>20 25 30    |
| Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile<br>35 40 45    |
| Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu<br>50 55 60    |
| Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr<br>65 70 75 80 |
| Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys<br>85 90 95    |

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Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr
 100 105 110

Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro
 115 120 125

Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr
 130 135 140

Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly
 145 150 155 160

Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu
 165 170 175

Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met
 180 185 190

Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile
 195 200 205

Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg
 210 215 220

Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu
 225 230 235 240

Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro
 245 250 255

Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly
 260 265 270

Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg
 275 280 285

Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu
 290 295 300

Ser Thr Thr Glu Trp Gln Ser Leu Ile Asn
 305 310

```

## (2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 961 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..958

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide

(B) LOCATION: 1..955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG GTG GGG AAC TGG GCT AAG GTT TTG GTT GTG ATG CTA CTC TTT GCC | 48  |
| Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala |     |
| 1 5 10 15                                                       |     |
| GGC GTC GAC GGG CAT ACC CGC GTG TCA GGA GGG GCA GCA GCC TCC GAT | 96  |
| Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ser Asp     |     |
| 20 25 30                                                        |     |
| ACC AGG GGC CTT GTG TCC CTC TTT AGC CCC GGG TCG GCT CAG AAA ATC | 144 |
| Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile |     |
| 35 40 45                                                        |     |
| CAG CTC GTA AAC ACC AAC GGC AGT TGG CAC ATC AAC AGG ACT GCC CTG | 192 |
| Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu |     |
| 50 55 60                                                        |     |
| AAC TGC AAC GAC TCC CTC CAA ACA GGG TTC TTT GCC GCA CTA TTC TAC | 240 |
| Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr |     |
| 65 70 75 80                                                     |     |
| AAA CAC AAA TTC AAC TCG TCT GGA TGC CCA GAG CGC TTG GCC AGC TGT | 288 |
| Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys |     |
| 85 90 95                                                        |     |
| CGC TCC ATC GAC AAG TTC GCT CAG GGG TGG GGT CCC CTC ACT TAC ACT | 336 |
| Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr |     |
| 100 105 110                                                     |     |
| GAG CCT AAC AGC TCG GAC CAG AGG CCC TAC TGC TGG CAC TAC GCG CCT | 384 |
| Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro |     |
| 115 120 125                                                     |     |
| CGA CCG TGT GGT ATT GTA CCC GCG TCT CAG GTG TGC GGT CCA GTG TAT | 432 |
| Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr |     |
| 130 135 140                                                     |     |
| TGC TTC ACC CCG AGC CCT GTT GTG GTG GGG ACG ACC GAT CGG TTT GGT | 480 |
| Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly |     |
| 145 150 155 160                                                 |     |
| GTC CCC ACG TAT AAC TGG GGG GCG AAC GAC TCG GAT GTG CTG ATT CTC | 528 |
| Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu |     |
| 165 170 175                                                     |     |
| AAC AAC ACG CGG CCG CCG CGA GGC AAC TGG TTC GGC TGT ACA TGG ATG | 576 |
| Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met |     |
| 180 185 190                                                     |     |
| AAT GGC ACT GGG TTC ACC AAG ACG TGT GGG GGC CCC CCG TGC AAC ATC | 624 |
| Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile |     |
| 195 200 205                                                     |     |
| GGG GGG GCC GGC AAC AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT CGG | 672 |
| Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg |     |
| 210 215 220                                                     |     |
| AAG CAC CCC GAG GCC ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG CTG | 720 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | His | Pro | Glu | Ala | Thr | Tyr | Ala | Arg | Cys | Gly | Ser | Gly | Pro | Trp | Leu |     |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| ACA | CCT | AGG | TGT | ATG | GTT | CAT | TAC | CCA | TAT | AGG | CTC | TGG | CAC | TAC | CCC | 768 |
| Thr | Pro | Arg | Cys | Met | Val | His | Tyr | Pro | Tyr | Arg | Leu | Trp | His | Tyr | Pro |     |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| TGC | ACT | GTC | AAC | TTC | ACC | ATC | TTC | AAG | GTT | AGG | ATG | TAC | GTG | GGG | GGC | 816 |
| Cys | Thr | Val | Asn | Phe | Thr | Ile | Phe | Lys | Val | Arg | Met | Tyr | Val | Gly | Gly |     |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| GTG | GAG | CAC | AGG | TTC | GAA | GCC | GCA | TGC | AAT | TGG | ACT | CGA | GGA | GAG | CGT | 864 |
| Val | Glu | His | Arg | Phe | Glu | Ala | Ala | Cys | Asn | Trp | Thr | Arg | Gly | Glu | Arg |     |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |     |
| TGT | GAC | TTG | GAG | GAC | AGG | GAT | AGA | TCA | GAG | CTT | AGC | CCG | CTG | CTG | CTG | 912 |
| Cys | Asp | Leu | Glu | Asp | Arg | Asp | Arg | Ser | Glu | Leu | Ser | Pro | Leu | Leu | Leu |     |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |
| TCT | ACA | ACA | GGT | GAT | CGA | GGG | CAG | ACA | CCA | TCA | CCA | CCA | TCA | CTA | A   | 958 |
| Ser | Thr | Thr | Gly | Asp | Arg | Gly | Gln | Thr | Pro | Ser | Pro | Pro | Ser | Leu |     |     |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     |     |
| TAG |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 961 |

## (2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 319 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Val | Gly | Asn | Trp | Ala | Lys | Val | Leu | Val | Val | Met | Leu | Leu | Phe | Ala |  |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Gly | Val | Asp | Gly | His | Thr | Arg | Val | Ser | Gly | Gly | Ala | Ala | Ala | Ser | Asp |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Thr | Arg | Gly | Leu | Val | Ser | Leu | Phe | Ser | Pro | Gly | Ser | Ala | Gln | Lys | Ile |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Gln | Leu | Val | Asn | Thr | Asn | Gly | Ser | Trp | His | Ile | Asn | Arg | Thr | Ala | Leu |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Asn | Cys | Asn | Asp | Ser | Leu | Gln | Thr | Gly | Phe | Phe | Ala | Ala | Leu | Phe | Tyr |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Lys | His | Lys | Phe | Asn | Ser | Ser | Gly | Cys | Pro | Glu | Arg | Leu | Ala | Ser | Cys |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Arg | Ser | Ile | Asp | Lys | Phe | Ala | Gln | Gly | Trp | Gly | Pro | Leu | Thr | Tyr | Thr |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Glu | Pro | Asn | Ser | Ser | Asp | Gln | Arg | Pro | Tyr | Cys | Trp | His | Tyr | Ala | Pro |  |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Arg | Pro | Cys | Gly | Ile | Val | Pro | Ala | Ser | Gln | Val | Cys | Gly | Pro | Val | Tyr |  |

|                                                                 |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|
| 130                                                             |     | 135 |     | 140 |
| Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly |     |     |     |     |
| 145                                                             |     | 150 | 155 | 160 |
| Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu |     |     |     |     |
|                                                                 | 165 |     | 170 | 175 |
| Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met |     |     |     |     |
|                                                                 | 180 |     | 185 | 190 |
| Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile |     |     |     |     |
|                                                                 | 195 |     | 200 | 205 |
| Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg |     |     |     |     |
|                                                                 | 210 |     | 215 | 220 |
| Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu |     |     |     |     |
| 225                                                             |     | 230 | 235 | 240 |
| Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro |     |     |     |     |
|                                                                 | 245 |     | 250 | 255 |
| Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly |     |     |     |     |
|                                                                 | 260 |     | 265 | 270 |
| Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg |     |     |     |     |
|                                                                 | 275 |     | 280 | 285 |
| Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu |     |     |     |     |
| 290                                                             |     | 295 | 300 |     |
| Ser Thr Thr Gly Asp Arg Gly Gln Thr Pro Ser Pro Pro Ser Leu     |     |     |     |     |
| 305                                                             |     | 310 | 315 |     |

## (2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1395 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1392

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..1389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG GGC CTC GCC TAC TAT

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ala | Gly | Ala | His | Trp | Gly | Val | Leu | Ala | Gly | Leu | Ala | Tyr | Tyr |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| TCC | ATG | GTG | GGG | AAC | TGG | GCT | AAG | GTT | TTG | GTT | GTG | ATG | CTA | CTC | TTT | 96  |
| Ser | Met | Val | Gly | Asn | Trp | Ala | Lys | Val | Leu | Val | Val | Met | Leu | Leu | Phe |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| GCC | GGC | GTC | GAC | GGG | CAT | ACC | CGC | GTG | TCA | GGA | GGG | GCA | GCA | GCC | TCC | 144 |
| Ala | Gly | Val | Asp | Gly | His | Thr | Arg | Val | Ser | Gly | Gly | Ala | Ala | Ala | Ser |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| GAT | ACC | AGG | GGC | CTT | GTG | TCC | CTC | TTT | AGC | CCC | GGG | TCG | GCT | CAG | AAA | 192 |
| Asp | Thr | Arg | Gly | Leu | Val | Ser | Leu | Phe | Ser | Pro | Gly | Ser | Ala | Gln | Lys |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| ATC | CAG | CTC | GTA | AAC | ACC | AAC | GGC | AGT | TGG | CAC | ATC | AAC | AGG | ACT | GCC | 240 |
| Ile | Gln | Leu | Val | Asn | Thr | Asn | Gly | Ser | Trp | His | Ile | Asn | Arg | Thr | Ala |     |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| CTG | AAC | TGC | AAC | GAC | TCC | CTC | CAA | ACA | GGG | TTC | TTT | GCC | GCA | CTA | TTC | 288 |
| Leu | Asn | Cys | Asn | Asp | Ser | Leu | Gln | Thr | Gly | Phe | Phe | Ala | Ala | Leu | Phe |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| TAC | AAA | CAC | AAA | TTC | AAC | TCG | TCT | GGA | TGC | CCA | GAG | CGC | TTG | GCC | AGC | 336 |
| Tyr | Lys | His | Lys | Phe | Asn | Ser | Ser | Gly | Cys | Pro | Glu | Arg | Leu | Ala | Ser |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| TGT | CGC | TCC | ATC | GAC | AAG | TTC | GCT | CAG | GGG | TGG | GGT | CCC | CTC | ACT | TAC | 384 |
| Cys | Arg | Ser | Ile | Asp | Lys | Phe | Ala | Gln | Gly | Trp | Gly | Pro | Leu | Thr | Tyr |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| ACT | GAG | CCT | AAC | AGC | TCG | GAC | CAG | AGG | CCC | TAC | TGC | TGG | CAC | TAC | GCG | 432 |
| Thr | Glu | Pro | Asn | Ser | Ser | Asp | Gln | Arg | Pro | Tyr | Cys | Trp | His | Tyr | Ala |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| CCT | CGA | CCG | TGT | GGT | ATT | GTA | CCC | GCG | TCT | CAG | GTG | TGC | GGT | CCA | GTG | 480 |
| Pro | Arg | Pro | Cys | Gly | Ile | Val | Pro | Ala | Ser | Gln | Val | Cys | Gly | Pro | Val |     |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| TAT | TGC | TTC | ACC | CCG | AGC | CCT | GTT | GTG | GTG | GGG | ACG | ACC | GAT | CGG | TTT | 528 |
| Tyr | Cys | Phe | Thr | Pro | Ser | Pro | Val | Val | Val | Gly | Thr | Thr | Asp | Arg | Phe |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| GGT | GTC | CCC | ACG | TAT | AAC | TGG | GGG | GCG | AAC | GAC | TCG | GAT | GTG | CTG | ATT | 576 |
| Gly | Val | Pro | Thr | Tyr | Asn | Trp | Gly | Ala | Asn | Asp | Ser | Asp | Val | Leu | Ile |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| CTC | AAC | AAC | ACG | CGG | CCG | CCG | CGA | GGC | AAC | TGG | TTC | GGC | TGT | ACA | TGG | 624 |
| Leu | Asn | Asn | Thr | Arg | Pro | Pro | Arg | Gly | Asn | Trp | Phe | Gly | Cys | Thr | Trp |     |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| ATG | AAT | GGC | ACT | GGG | TTC | ACC | AAG | ACG | TGT | GGG | GGC | CCC | CCG | TGC | AAC | 672 |
| Met | Asn | Gly | Thr | Gly | Phe | Thr | Lys | Thr | Cys | Gly | Gly | Pro | Pro | Cys | Asn |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| ATC | GGG | GGG | GCC | GGC | AAC | AAC | ACC | TTG | ACC | TGC | CCC | ACT | GAC | TGT | TTT | 720 |
| Ile | Gly | Gly | Ala | Gly | Asn | Asn | Thr | Leu | Thr | Cys | Pro | Thr | Asp | Cys | Phe |     |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| CGG | AAG | CAC | CCC | GAG | GCC | ACC | TAC | GCC | AGA | TGC | GGT | TCT | GGG | CCC | TGG | 768 |
| Arg | Lys | His | Pro | Glu | Ala | Thr | Tyr | Ala | Arg | Cys | Gly | Ser | Gly | Pro | Trp |     |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| CTG ACA CCT AGG TGT ATG GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC    | 816  |
| Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr    |      |
| 260 265 270                                                        |      |
| CCC TGC ACT GTC AAC TTC ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG    | 864  |
| Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly    |      |
| 275 280 285                                                        |      |
| GGC GTG GAG CAC AGG TTC GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG    | 912  |
| Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu    |      |
| 290 295 300                                                        |      |
| CGT TGT GAC TTG GAG GAC AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG    | 960  |
| Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu    |      |
| 305 310 315 320                                                    |      |
| CTG TCT ACA ACA GAG TGG CAG ATA CTG CCC TGT TCC TTC ACC ACC CTG    | 1008 |
| Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu    |      |
| 325 330 335                                                        |      |
| CCG GCC CTA TCC ACC GGC CTG ATC CAC CTC CAT CAG AAC ATC GTG GAC    | 1056 |
| Pro Ala Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp    |      |
| 340 345 350                                                        |      |
| GTG CAA TAC CTG TAC GGT GTA GGG TCG GCG GTT GTC TCC CTT GTC ATC    | 1104 |
| Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val Val Ser Leu Val Ile    |      |
| 355 360 365                                                        |      |
| AAA TGG GAG TAT GTC CTG TTG CTC TTC CTT CTC CTG GCA GAC GCG CGC    | 1152 |
| Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg    |      |
| 370 375 380                                                        |      |
| ATC TGC GCC TGC TTA TGG ATG ATG CTG CTG ATA GCT CAA GCT GAG GCC    | 1200 |
| Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala    |      |
| 385 390 395 400                                                    |      |
| GCC TTA GAG AAC CTG GTG GTC CTC AAT GCG GCG GCC GTG GCC GGG GCG    | 1248 |
| Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala Ala Val Ala Gly Ala    |      |
| 405 410 415                                                        |      |
| CAT GGC ACT CTT TCC TTC CTT GTG TTC TTC TGT GCT GCC TGG TAC ATC    | 1296 |
| His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile    |      |
| 420 425 430                                                        |      |
| AAG GGC AGG CTG GTC CCT GGT GCG GCA TAC GCC TTC TAT GGC GTG TGG    | 1344 |
| Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp    |      |
| 435 440 445                                                        |      |
| CCG CTG CTC CTG CTT CTG CTG GCC TTA CCA CCA CGA GCT TAT GCC TAGTAA | 1395 |
| Pro Leu Leu Leu Leu Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala        |      |
| 450 455 460                                                        |      |

## (2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 463 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```

Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr
 1 5 10 15

Ser Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe
 20 25 30
Ala Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser
 35 40 45

Asp Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys
 50 55 60

Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala
 65 70 75 80

Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe
 85 90 95

Tyr Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser
 100 105 110

Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr
 115 120 125

Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala
 130 135 140

Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val
 145 150 155 160

Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe
 165 170 175

Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile
 180 185 190

Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp
 195 200 205

Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn
 210 215 220

Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe
 225 230 235 240

Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp
 245 250 255

Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr
 260 265 270

Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly
 275 280 285

Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu
 290 295 300

Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu
 305 310 315 320

```

Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu  
 325 330 335  
 Pro Ala Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp  
 340 345 350  
 Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val Val Ser Leu Val Ile  
 355 360 365  
 Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg  
 370 375 380  
 Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala  
 385 390 395 400  
 Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala Val Ala Gly Ala  
 405 410 415  
 His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile  
 420 425 430  
 Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp  
 435 440 445  
 Pro Leu Leu Leu Leu Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala  
 450 455 460

## (2) INFORMATION FOR SEQ ID NO: 47:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2079

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..2076

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

AAT TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC  
 Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu  
 1 5 10 15

48

GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG  
 Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg  
 20 25 30

96

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GCC | CTG | GCG | CAT | GGC | GTC | CGG | GTT | CTG | GAG | GAC | GGC | GTG | AAC | TAT | GCA | 144 |
| Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| ACA | GGG | AAT | TTG | CCC | GGT | TGC | TCT | TTC | TCT | ATC | TTC | CTC | TTG | GCT | TTG | 192 |
| Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| CTG | TCC | TGT | CTG | ACC | GTT | CCA | GCT | TCC | GCT | TAT | GAA | GTG | CGC | AAC | GTG | 240 |
| Leu | Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser | Ala | Tyr | Glu | Val | Arg | Asn | Val |     |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| TCC | GGG | ATG | TAC | CAT | GTC | ACG | AAC | GAC | TGC | TCC | AAC | TCA | AGC | ATT | GTG | 288 |
| Ser | Gly | Met | Tyr | His | Val | Thr | Asn | Asp | Cys | Ser | Asn | Ser | Ser | Ile | Val |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| TAT | GAG | GCA | GCG | GAC | ATG | ATC | ATG | CAC | ACC | CCC | GGG | TGC | GTG | CCC | TGC | 336 |
| Tyr | Glu | Ala | Ala | Asp | Met | Ile | Met | His | Thr | Pro | Gly | Cys | Val | Pro | Cys |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| GTT | CGG | GAG | AAC | AAC | TCT | TCC | CGC | TGC | TGG | GTA | GCG | CTC | ACC | CCC | ACG | 384 |
| Val | Arg | Glu | Asn | Asn | Ser | Ser | Arg | Cys | Trp | Val | Ala | Leu | Thr | Pro | Thr |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| CTC | GCA | GCT | AGG | AAC | GCC | AGC | GTC | CCC | ACC | ACG | ACA | ATA | CGA | CGC | CAC | 432 |
| Leu | Ala | Ala | Arg | Asn | Ala | Ser | Val | Pro | Thr | Thr | Thr | Ile | Arg | Arg | His |     |
|     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| GTC | GAT | TTG | CTC | GTT | GGG | GCG | GCT | GCT | TTC | TGT | TCC | GCT | ATG | TAC | GTG | 480 |
| Val | Asp | Leu | Leu | Val | Gly | Ala | Ala | Ala | Phe | Cys | Ser | Ala | Met | Tyr | Val |     |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| GGG | GAC | CTC | TGC | GGA | TCT | GTC | TTC | CTC | GTC | TCC | CAG | CTG | TTC | ACC | ATC | 528 |
| Gly | Asp | Leu | Cys | Gly | Ser | Val | Phe | Leu | Val | Ser | Gln | Leu | Phe | Thr | Ile |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| TCG | CCT | CGC | CGG | CAT | GAG | ACG | GTG | CAG | GAC | TGC | AAT | TGC | TCA | ATC | TAT | 576 |
| Ser | Pro | Arg | Arg | His | Glu | Thr | Val | Gln | Asp | Cys | Asn | Cys | Ser | Ile | Tyr |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| CCC | GGC | CAC | ATA | ACG | GGT | CAC | CGT | ATG | GCT | TGG | GAT | ATG | ATG | ATG | AAC | 624 |
| Pro | Gly | His | Ile | Thr | Gly | His | Arg | Met | Ala | Trp | Asp | Met | Met | Met | Asn |     |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| TGG | TCG | CCT | ACA | ACG | GCC | CTG | GTG | GTA | TCG | CAG | CTG | CTC | CGG | ATC | CCA | 672 |
| Trp | Ser | Pro | Thr | Thr | Ala | Leu | Val | Val | Ser | Gln | Leu | Leu | Arg | Ile | Pro |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| CAA | GCT | GTC | GTG | GAC | ATG | GTG | GCG | GGG | GCC | CAT | TGG | GGA | GTC | CTG | GCG | 720 |
| Gln | Ala | Val | Val | Asp | Met | Val | Ala | Gly | Ala | His | Trp | Gly | Val | Leu | Ala |     |
|     | 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| GGC | CTC | GCC | TAC | TAT | TCC | ATG | GTG | GGG | AAC | TGG | GCT | AAG | GTT | TTG | GTT | 768 |
| Gly | Leu | Ala | Tyr | Tyr | Ser | Met | Val | Gly | Asn | Trp | Ala | Lys | Val | Leu | Val |     |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| GTG | ATG | CTA | CTC | TTT | GCC | GGC | GTC | GAC | GGG | CAT | ACC | CGC | GTG | TCA | GGA | 816 |
| Val | Met | Leu | Leu | Phe | Ala | Gly | Val | Asp | Gly | His | Thr | Arg | Val | Ser | Gly |     |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| GGG | GCA | GCA | GCC | TCC | GAT | ACC | AGG | GGC | CTT | GTG | TCC | CTC | TTT | AGC | CCC | 864 |
| Gly | Ala | Ala | Ala | Ser | Asp | Thr | Arg | Gly | Leu | Val | Ser | Leu | Phe | Ser | Pro |     |

| 275                                                                                                                                                   | 280 | 285 |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----|------|
| GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC AAC GGC AGT TGG CAC<br>Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His<br>290 295 300     |     |     | 912  |
| ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC CTC CAA ACA GGG TTC<br>Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe<br>305 310 315 320 |     |     | 960  |
| TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC TCG TCT GGA TGC CCA<br>Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly Cys Pro<br>325 330 335     |     |     | 1008 |
| GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG TTC GCT CAG GGG TGG<br>Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp<br>340 345 350     |     |     | 1056 |
| GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG GAC CAG AGG CCC TAC<br>Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr<br>355 360 365     |     |     | 1104 |
| TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT ATT GTA CCC GCG TCT CAG<br>Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln<br>370 375 380     |     |     | 1152 |
| GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC CCT GTT GTG GTG GGG<br>Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly<br>385 390 395 400 |     |     | 1200 |
| ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT AAC TGG GGG GCG AAC GAC<br>Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp<br>405 410 415     |     |     | 1248 |
| TCG GAT GTG CTG ATT CTC AAC AAC ACG CGG CCG CCG CGA GGC AAC TGG<br>Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp<br>420 425 430     |     |     | 1296 |
| TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC ACC AAG ACG TGT GGG<br>Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly<br>435 440 445     |     |     | 1344 |
| GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC AAC ACC TTG ACC TGC<br>Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys<br>450 455 460     |     |     | 1392 |
| CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG GCC ACC TAC GCC AGA TGC<br>Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys<br>465 470 475 480 |     |     | 1440 |
| GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG GTT CAT TAC CCA TAT<br>Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr<br>485 490 495     |     |     | 1488 |
| AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC ACC ATC TTC AAG GTT<br>Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val<br>500 505 510     |     |     | 1536 |
| AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC GAA GCC GCA TGC AAT<br>Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn<br>515 520 525     |     |     | 1584 |
| TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC AGG GAT AGA TCA GAG                                                                                       |     |     | 1632 |

|     |     |     |     |        |     |     |     |     |     |     |     |     |     |     |     |      |  |
|-----|-----|-----|-----|--------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Trp | Thr | Arg | Gly | Glu    | Arg | Cys | Asp | Leu | Glu | Asp | Arg | Asp | Arg | Ser | Glu |      |  |
| 530 |     |     |     |        |     | 535 |     |     |     |     | 540 |     |     |     |     |      |  |
| CTT | AGC | CCG | CTG | CTG    | CTG | TCT | ACA | ACA | GAG | TGG | CAG | ATA | CTG | CCC | TGT | 1680 |  |
| Leu | Ser | Pro | Leu | Leu    | Leu | Ser | Thr | Thr | Glu | Trp | Gln | Ile | Leu | Pro | Cys |      |  |
| 545 |     |     |     |        | 550 |     |     |     |     | 555 |     |     |     |     | 560 |      |  |
| TCC | TTC | ACC | ACC | CTG    | CCG | GCC | CTA | TCC | ACC | GGC | CTG | ATC | CAC | CTC | CAT | 1728 |  |
| Ser | Phe | Thr | Thr |        | Leu | Pro | Ala | Leu | Ser | Thr | Gly | Leu | Ile | His | Leu | His  |  |
|     |     |     |     | 565    |     |     |     |     | 570 |     |     |     |     | 575 |     |      |  |
| CAG | AAC | ATC | GTG | GAC    | GTG | CAA | TAC | CTG | TAC | GGT | GTA | GGG | TCG | GCG | GTT | 1776 |  |
| Gln | Asn | Ile | Val | Asp    | Val | Gln | Tyr | Leu | Tyr | Gly | Val | Gly | Ser | Ala | Val |      |  |
|     |     |     | 580 |        |     |     |     | 585 |     |     |     |     | 590 |     |     |      |  |
| GTC | TCC | CTT | GTC | ATC    | AAA | TGG | GAG | TAT | GTC | CTG | TTG | CTC | TTC | CTT | CTC | 1824 |  |
| Val | Ser |     | Leu | Val    | Ile | Lys | Trp | Glu | Tyr | Val | Leu | Leu | Leu | Phe | Leu | Leu  |  |
|     |     | 595 |     |        |     |     | 600 |     |     |     |     | 605 |     |     |     |      |  |
| CTG | GCA | GAC | GCG | CGC    | ATC | TGC | GCC | TGC | TTA | TGG | ATG | ATG | CTG | CTG | ATA | 1872 |  |
| Leu | Ala | Asp | Ala | Arg    | Ile | Cys | Ala | Cys | Leu | Trp | Met | Met | Leu | Leu | Ile |      |  |
|     | 610 |     |     |        |     | 615 |     |     |     |     | 620 |     |     |     |     |      |  |
| GCT | CAA | GCT | GAG | GCC    | GCC | TTA | GAG | AAC | CTG | GTG | GTC | CTC | AAT | GCG | GCG | 1920 |  |
| Ala | Gln | Ala | Glu | Ala    | Ala | Leu | Glu | Asn | Leu | Val | Val | Leu | Asn | Ala | Ala |      |  |
| 625 |     |     |     |        | 630 |     |     |     |     | 635 |     |     |     |     | 640 |      |  |
| GCC | GTG | GCC | GGG | GCG    | CAT | GGC | ACT | CTT | TCC | TTC | CTT | GTG | TTC | TTC | TGT | 1968 |  |
| Ala | Val | Ala | Gly | Ala    | His | Gly | Thr | Leu | Ser | Phe | Leu | Val | Phe | Phe | Cys |      |  |
|     |     |     |     | 645    |     |     |     |     | 650 |     |     |     |     | 655 |     |      |  |
| GCT | GCC | TGG | TAC | ATC    | AAG | GGC | AGG | CTG | GTC | CCT | GGT | GCG | GCA | TAC | GCC | 2016 |  |
| Ala | Ala | Trp | Tyr | Ile    | Lys | Gly | Arg | Leu | Val | Pro | Gly | Ala | Ala | Tyr | Ala |      |  |
|     |     |     | 660 |        |     |     |     | 665 |     |     |     |     | 670 |     |     |      |  |
| TTC | TAT | GGC | GTG | TGG    | CCG | CTG | CTC | CTG | CTT | CTG | CTG | GCC | TTA | CCA | CCA | 2064 |  |
| Phe | Tyr | Gly | Val | Trp    | Pro | Leu | Leu | Leu | Leu | Leu | Leu | Ala | Leu | Pro | Pro |      |  |
|     |     | 675 |     |        |     | 680 |     |     |     |     |     | 685 |     |     |     |      |  |
| CGA | GCT | TAT | GCC | TAGTAA |     |     |     |     |     |     |     |     |     |     |     | 2082 |  |
| Arg | Ala | Tyr | Ala |        |     |     |     |     |     |     |     |     |     |     |     |      |  |
|     |     |     | 690 |        |     |     |     |     |     |     |     |     |     |     |     |      |  |

## (2) INFORMATION FOR SEQ ID NO: 48:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Asn | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Val | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu | Gly | Gly | Ala | Ala | Arg |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala |  |  |

35

40

45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu  
 50 55 60  
 Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val  
 65 70 75 80  
 Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val  
 85 90 95  
 Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys  
 100 105 110  
 Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr  
 115 120 125  
 Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His  
 130 135 140  
 Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val  
 145 150 155 160  
 Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile  
 165 170 175  
 Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr  
 180 185 190  
 Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn  
 195 200 205  
 Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro  
 210 215 220  
 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala  
 225 230 235 240  
 Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Val  
 245 250 255  
 Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val Ser Gly  
 260 265 270  
 Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe Ser Pro  
 275 280 285  
 Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His  
 290 295 300  
 Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe  
 305 310 315 320  
 Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly Cys Pro  
 325 330 335  
 Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp  
 340 345 350  
 Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr  
 355 360 365  
 Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln

[illegible]

## (2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2433 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..2430

- (ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..2427

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC | 48  |
| Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn |     |
| 1 5 10 15                                                       |     |
| CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT GGT | 96  |
| Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly |     |
| 20 25 30                                                        |     |
| GGA GTT TAC CTG TTG CCG CGC AGG GGC CCC AGG TTG GGT GTG CGC GCG | 144 |
| Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala |     |
| 35 40 45                                                        |     |
| ACT AGG AAG ACT TCC GAG CGG TCG CAA CCT CGT GGG AGG CGA CAA CCT | 192 |
| Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro |     |
| 50 55 60                                                        |     |
| ATC CCC AAG GCT CGC CGA CCC GAG GGT AGG GCC TGG GCT CAG CCC GGG | 240 |
| Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly |     |
| 65 70 75 80                                                     |     |
| TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC ATG GGG TGG GCA GGA TGG | 288 |
| Tyr Pro Trp Pro Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp     |     |
| 85 90 95                                                        |     |
| CTC CTG TCA CCC CGC GGC TCT CGG CCT AGT TGG GGC CCT ACA GAC CCC | 336 |
| Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro |     |
| 100 105 110                                                     |     |
| CGG CGT AGG TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC | 384 |
| Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys |     |
| 115 120 125                                                     |     |
| GGC TTC GCC GAC CTC GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA | 432 |
| Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu |     |
| 130 135 140                                                     |     |
| GGG GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC | 480 |



|                   |            |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |            |                   |      |
|-------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|------|
| Gly<br>145        | Gly        | Ala               | Ala               | Arg               | Ala<br>150        | Leu               | Ala               | His               | Gly               | Val<br>155        | Arg               | Val               | Leu               | Glu        | Asp<br>160        |      |
| GGC<br>Gly        | GTG<br>Val | AAC<br>Asn        | TAT<br>Tyr        | GCA<br>Ala<br>165 | ACA<br>Thr        | GGG<br>Gly        | AAT<br>Asn        | TTG<br>Leu        | CCC<br>Pro        | GGT<br>Gly        | TGC<br>Cys        | TCT<br>Ser        | TTC<br>Phe        | TCT<br>Ser | ATC<br>Ile        | 528  |
| TTC<br>Phe        | CTC<br>Leu | TTG<br>Leu        | GCT<br>Ala<br>180 | TTG<br>Leu        | CTG<br>Leu        | TCC<br>Ser        | TGT<br>Cys        | CTG<br>Leu<br>185 | ACC<br>Thr        | GTT<br>Val        | CCA<br>Pro        | GCT<br>Ala        | TCC<br>Ser        | GCT<br>Ala | TAT<br>Tyr        | 576  |
| GAA<br>Glu        | GTG<br>Val | CGC<br>Arg        | AAC<br>Asn<br>195 | GTG<br>Val        | TCC<br>Ser        | GGG<br>Gly        | ATG<br>Met<br>200 | TAC<br>Tyr        | CAT<br>His        | GTC<br>Val        | ACG<br>Thr        | AAC<br>Asn<br>205 | GAC<br>Asp        | TGC<br>Cys | TCC<br>Ser        | 624  |
| AAC<br>Asn<br>210 | TCA<br>Ser | AGC<br>Ser        | ATT<br>Ile        | GTG<br>Val        | TAT<br>Tyr        | GAG<br>Glu<br>215 | GCA<br>Ala        | GCG<br>Ala        | GAC<br>Asp        | ATG<br>Met        | ATC<br>Ile        | ATG<br>Met        | CAC<br>His        | ACC<br>Thr | CCC<br>Pro        | 672  |
| GGG<br>Gly<br>225 | TGC<br>Cys | GTG<br>Val        | CCC<br>Pro        | TGC<br>Cys        | GTT<br>Val<br>230 | CGG<br>Arg        | GAG<br>Glu        | AAC<br>Asn        | AAC<br>Asn        | TCT<br>Ser<br>235 | TCC<br>Ser        | CGC<br>Arg        | TGC<br>Cys        | TGG<br>Trp | GTA<br>Val<br>240 | 720  |
| GCG<br>Ala        | CTC<br>Leu | ACC<br>Thr        | CCC<br>Pro        | ACG<br>Thr<br>245 | CTC<br>Leu        | GCA<br>Ala        | GCT<br>Ala        | AGG<br>Arg        | AAC<br>Asn<br>250 | GCC<br>Ala        | AGC<br>Ser        | GTC<br>Val        | CCC<br>Pro        | ACC<br>Thr | ACG<br>Thr        | 768  |
| ACA<br>Thr        | ATA<br>Ile | CGA<br>Arg        | CGC<br>Arg<br>260 | CAC<br>His        | GTC<br>Val        | GAT<br>Asp        | TTG<br>Leu        | CTC<br>Leu<br>265 | GTT<br>Val        | GGG<br>Gly        | GCG<br>Ala        | GCT<br>Ala        | GCT<br>Ala        | TTC<br>Phe | TGT<br>Cys        | 816  |
| TCC<br>Ser        | GCT<br>Ala | ATG<br>Met<br>275 | TAC<br>Tyr        | GTG<br>Val        | GGG<br>Gly        | GAC<br>Asp        | CTC<br>Leu<br>280 | TGC<br>Cys        | GGA<br>Gly        | TCT<br>Ser        | GTC<br>Val        | TTC<br>Phe        | CTC<br>Leu        | GTC<br>Val | TCC<br>Ser        | 864  |
| CAG<br>Gln<br>290 | CTG<br>Leu | TTC<br>Phe        | ACC<br>Thr        | ATC<br>Ile        | TCG<br>Ser        | CCT<br>Pro        | CGC<br>Arg        | CGG<br>Arg        | CAT<br>His        | GAG<br>Glu        | ACG<br>Thr        | GTG<br>Val        | CAG<br>Gln        | GAC<br>Asp | TGC<br>Cys        | 912  |
| AAT<br>Asn<br>305 | TGC<br>Cys | TCA<br>Ser        | ATC<br>Ile        | TAT<br>Tyr        | CCC<br>Pro<br>310 | GGC<br>Gly        | CAC<br>His        | ATA<br>Ile        | ACG<br>Thr        | GGT<br>Gly<br>315 | CAC<br>His        | CGT<br>Arg        | ATG<br>Met        | GCT<br>Ala | TGG<br>Trp<br>320 | 960  |
| GAT<br>Asp        | ATG<br>Met | ATG<br>Met        | ATG<br>Met        | AAC<br>Asn<br>325 | TGG<br>Trp        | TCG<br>Ser        | CCT<br>Pro        | ACA<br>Thr        | ACG<br>Thr        | GCC<br>Ala<br>330 | CTG<br>Leu        | GTG<br>Val        | GTA<br>Val        | TCG<br>Ser | CAG<br>Gln        | 1008 |
| CTG<br>Leu        | CTC<br>Leu | CGG<br>Arg        | ATC<br>Ile<br>340 | CCA<br>Pro        | CAA<br>Gln        | GCT<br>Ala        | GTC<br>Val        | GTG<br>Val<br>345 | GAC<br>Asp        | ATG<br>Met        | GTG<br>Val        | GCG<br>Ala        | GGG<br>Gly<br>350 | GCC<br>Ala | CAT<br>His        | 1056 |
| TGG<br>Trp        | GGA<br>Gly | GTC<br>Val        | CTG<br>Leu        | GCG<br>Ala        | GGC<br>Gly        | CTC<br>Leu        | GCC<br>Ala        | TAC<br>Tyr<br>360 | TAT<br>Tyr        | TCC<br>Ser        | ATG<br>Met        | GTG<br>Val        | GGG<br>Gly        | AAC<br>Asn | TGG<br>Trp        | 1104 |
| GCT<br>Ala<br>370 | AAG<br>Lys | GTT<br>Val        | TTG<br>Leu        | GTT<br>Val        | GTG<br>Val        | ATG<br>Met<br>375 | CTA<br>Leu        | CTC<br>Leu        | TTT<br>Phe        | GCC<br>Ala        | GGC<br>Gly<br>380 | GTC<br>Val        | GAC<br>Asp        | GGG<br>Gly | CAT<br>His        | 1152 |
| ACC<br>Thr<br>385 | CGC<br>Arg | GTG<br>Val        | TCA<br>Ser        | GGA<br>Gly        | GGG<br>Gly<br>390 | GCA<br>Ala        | GCA<br>Ala        | GCC<br>Ala        | TCC<br>Ser        | GAT<br>Asp<br>395 | ACC<br>Thr        | AGG<br>Arg        | GGC<br>Gly        | CTT<br>Leu | GTG<br>Val<br>400 | 1200 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| TCC | CTC | TTT | AGC | CCC | GGG | TCG | GCT | CAG | AAA | ATC | CAG | CTC | GTA | AAC | ACC | 1248 |
| Ser | Leu | Phe | Ser | Pro | Gly | Ser | Ala | Gln | Lys | Ile | Gln | Leu | Val | Asn | Thr |      |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |      |
| AAC | GGC | AGT | TGG | CAC | ATC | AAC | AGG | ACT | GCC | CTG | AAC | TGC | AAC | GAC | TCC | 1296 |
| Asn | Gly | Ser | Trp | His | Ile | Asn | Arg | Thr | Ala | Leu | Asn | Cys | Asn | Asp | Ser |      |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |      |
| CTC | CAA | ACA | GGG | TTC | TTT | GCC | GCA | CTA | TTC | TAC | AAA | CAC | AAA | TTC | AAC | 1344 |
| Leu | Gln | Thr | Gly | Phe | Phe | Ala | Ala | Leu | Phe | Tyr | Lys | His | Lys | Phe | Asn |      |
|     |     |     | 435 |     |     |     | 440 |     |     |     |     | 445 |     |     |     |      |
| TCG | TCT | GGA | TGC | CCA | GAG | CGC | TTG | GCC | AGC | TGT | CGC | TCC | ATC | GAC | AAG | 1392 |
| Ser | Ser | Gly | Cys | Pro | Glu | Arg | Leu | Ala | Ser | Cys | Arg | Ser | Ile | Asp | Lys |      |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |      |
| TTC | GCT | CAG | GGG | TGG | GGT | CCC | CTC | ACT | TAC | ACT | GAG | CCT | AAC | AGC | TCG | 1440 |
| Phe | Ala | Gln | Gly | Trp | Gly | Pro | Leu | Thr | Tyr | Thr | Glu | Pro | Asn | Ser | Ser |      |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |      |
| GAC | CAG | AGG | CCC | TAC | TGC | TGG | CAC | TAC | GCG | CCT | CGA | CCG | TGT | GGT | ATT | 1488 |
| Asp | Gln | Arg | Pro | Tyr | Cys | Trp | His | Tyr | Ala | Pro | Arg | Pro | Cys | Gly | Ile |      |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |      |
| GTA | CCC | GCG | TCT | CAG | GTG | TGC | GGT | CCA | GTG | TAT | TGC | TTC | ACC | CCG | AGC | 1536 |
| Val | Pro | Ala | Ser | Gln | Val | Cys | Gly | Pro | Val | Tyr | Cys | Phe | Thr | Pro | Ser |      |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |      |
| CCT | GTT | GTG | GTG | GGG | ACG | ACC | GAT | CGG | TTT | GGT | GTC | CCC | ACG | TAT | AAC | 1584 |
| Pro | Val | Val | Val | Gly | Thr | Thr | Asp | Arg | Phe | Gly | Val | Pro | Thr | Tyr | Asn |      |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |      |
| TGG | GGG | GCG | AAC | GAC | TCG | GAT | GTG | CTG | ATT | CTC | AAC | AAC | ACG | CGG | CCG | 1632 |
| Trp | Gly | Ala | Asn | Asp | Ser | Asp | Val | Leu | Ile | Leu | Asn | Asn | Thr | Arg | Pro |      |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |      |
| CCG | CGA | GGC | AAC | TGG | TTC | GGC | TGT | ACA | TGG | ATG | AAT | GGC | ACT | GGG | TTC | 1680 |
| Pro | Arg | Gly | Asn | Trp | Phe | Gly | Cys | Thr | Trp | Met | Asn | Gly | Thr | Gly | Phe |      |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |      |
| ACC | AAG | ACG | TGT | GGG | GGC | CCC | CCG | TGC | AAC | ATC | GGG | GGG | GCC | GGC | AAC | 1728 |
| Thr | Lys | Thr | Cys | Gly | Gly | Pro | Pro | Cys | Asn | Ile | Gly | Gly | Ala | Gly | Asn |      |
|     |     |     |     | 565 |     |     |     | 570 |     |     |     |     | 575 |     |     |      |
| AAC | ACC | TTG | ACC | TGC | CCC | ACT | GAC | TGT | TTT | CGG | AAG | CAC | CCC | GAG | GCC | 1776 |
| Asn | Thr | Leu | Thr | Cys | Pro | Thr | Asp | Cys | Phe | Arg | Lys | His | Pro | Glu | Ala |      |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |      |
| ACC | TAC | GCC | AGA | TGC | GGT | TCT | GGG | CCC | TGG | CTG | ACA | CCT | AGG | TGT | ATG | 1824 |
| Thr | Tyr | Ala | Arg | Cys | Gly | Ser | Gly | Pro | Trp | Leu | Thr | Pro | Arg | Cys | Met |      |
|     |     | 595 |     |     |     | 600 |     |     |     |     |     | 605 |     |     |     |      |
| GTT | CAT | TAC | CCA | TAT | AGG | CTC | TGG | CAC | TAC | CCC | TGC | ACT | GTC | AAC | TTC | 1872 |
| Val | His | Tyr | Pro | Tyr | Arg | Leu | Trp | His | Tyr | Pro | Cys | Thr | Val | Asn | Phe |      |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |      |
| ACC | ATC | TTC | AAG | GTT | AGG | ATG | TAC | GTG | GGG | GGC | GTG | GAG | CAC | AGG | TTC | 1920 |
| Thr | Ile | Phe | Lys | Val | Arg | Met | Tyr | Val | Gly | Gly | Val | Glu | His | Arg | Phe |      |
|     | 625 |     |     |     | 630 |     |     |     | 635 |     |     |     |     |     | 640 |      |
| GAA | GCC | GCA | TGC | AAT | TGG | ACT | CGA | GGA | GAG | CGT | TGT | GAC | TTG | GAG | GAC | 1968 |

|     |     |     |     |     |     |     |     |     |        |     |     |     |     |     |     |      |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|--------|-----|-----|-----|-----|-----|-----|------|--|
| Glu | Ala | Ala | Cys | Asn | Trp | Thr | Arg | Gly | Glu    | Arg | Cys | Asp | Leu | Glu | Asp |      |  |
|     |     |     |     | 645 |     |     |     |     | 650    |     |     |     |     | 655 |     |      |  |
| AGG | GAT | AGA | TCA | GAG | CTT | AGC | CCG | CTG | CTG    | CTG | TCT | ACA | ACA | GAG | TGG | 2016 |  |
| Arg | Asp | Arg | Ser | Glu | Leu | Ser | Pro | Leu | Leu    | Leu | Ser | Thr | Thr | Glu | Trp |      |  |
|     |     |     | 660 |     |     |     |     | 665 |        |     |     |     |     | 670 |     |      |  |
| CAG | ATA | CTG | CCC | TGT | TCC | TTC | ACC | ACC | CTG    | CCG | GCC | CTA | TCC | ACC | GGC | 2064 |  |
| Gln | Ile | Leu | Pro | Cys | Ser | Phe | Thr | Thr | Leu    | Pro | Ala | Leu | Ser | Thr | Gly |      |  |
|     |     |     | 675 |     |     |     | 680 |     |        |     |     | 685 |     |     |     |      |  |
| CTG | ATC | CAC | CTC | CAT | CAG | AAC | ATC | GTG | GAC    | GTG | CAA | TAC | CTG | TAC | GGT | 2112 |  |
| Leu | Ile | His | Leu | His | Gln | Asn | Ile | Val | Asp    | Val | Gln | Tyr | Leu | Tyr | Gly |      |  |
|     |     |     | 690 |     |     | 695 |     |     |        |     | 700 |     |     |     |     |      |  |
| GTA | GGG | TCG | GCG | GTT | GTC | TCC | CTT | GTC | ATC    | AAA | TGG | GAG | TAT | GTC | CTG | 2160 |  |
| Val | Gly | Ser | Ala | Val | Val | Ser | Leu | Val | Ile    | Lys | Trp | Glu | Tyr | Val | Leu |      |  |
| 705 |     |     |     |     | 710 |     |     |     |        | 715 |     |     |     |     | 720 |      |  |
| TTG | CTC | TTC | CTT | CTC | CTG | GCA | GAC | GCG | CGC    | ATC | TGC | GCC | TGC | TTA | TGG | 2208 |  |
| Leu | Leu | Phe | Leu | Leu | Leu | Ala | Asp | Ala | Arg    | Ile | Cys | Ala | Cys | Leu | Trp |      |  |
|     |     |     |     | 725 |     |     |     | 730 |        |     |     |     |     | 735 |     |      |  |
| ATG | ATG | CTG | CTG | ATA | GCT | CAA | GCT | GAG | GCC    | GCC | TTA | GAG | AAC | CTG | GTG | 2256 |  |
| Met | Met | Leu | Leu | Ile | Ala | Gln | Ala | Glu | Ala    | Ala | Leu | Glu | Asn | Leu | Val |      |  |
|     |     |     | 740 |     |     |     |     | 745 |        |     |     |     | 750 |     |     |      |  |
| GTC | CTC | AAT | GCG | GCG | GCC | GTG | GCC | GGG | GCG    | CAT | GGC | ACT | CTT | TCC | TTC | 2304 |  |
| Val | Leu | Asn | Ala | Ala | Ala | Val | Ala | Gly | Ala    | His | Gly | Thr | Leu | Ser | Phe |      |  |
|     |     | 755 |     |     |     | 760 |     |     |        |     | 765 |     |     |     |     |      |  |
| CTT | GTG | TTC | TTC | TGT | GCT | GCC | TGG | TAC | ATC    | AAG | GGC | AGG | CTG | GTC | CCT | 2352 |  |
| Leu | Val | Phe | Phe | Cys | Ala | Ala | Trp | Tyr | Ile    | Lys | Gly | Arg | Leu | Val | Pro |      |  |
|     |     | 770 |     |     | 775 |     |     |     |        |     | 780 |     |     |     |     |      |  |
| GGT | GCG | GCA | TAC | GCC | TTC | TAT | GGC | GTG | TGG    | CCG | CTG | CTC | CTG | CTT | CTG | 2400 |  |
| Gly | Ala | Ala | Tyr | Ala | Phe | Tyr | Gly | Val | Trp    | Pro | Leu | Leu | Leu | Leu | Leu |      |  |
| 785 |     |     |     | 790 |     |     |     | 795 |        |     |     |     |     |     | 800 |      |  |
| CTG | GCC | TTA | CCA | CCA | CGA | GCT | TAT | GCC | TAGTAA |     |     |     |     |     |     | 2433 |  |
| Leu | Ala | Leu | Pro | Pro | Arg | Ala | Tyr | Ala |        |     |     |     |     |     |     |      |  |
|     |     |     | 805 |     |     |     |     | 810 |        |     |     |     |     |     |     |      |  |

## (2) INFORMATION FOR SEQ ID NO: 50:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Ser | Thr | Asn | Pro | Lys | Pro | Gln | Arg | Lys | Thr | Lys | Arg | Asn | Thr | Asn |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Arg | Arg | Pro | Gln | Asp | Val | Lys | Phe | Pro | Gly | Gly | Gly | Gln | Ile | Val | Gly |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Gly | Val | Tyr | Leu | Leu | Pro | Arg | Arg | Gly | Pro | Arg | Leu | Gly | Val | Arg | Ala |  |  |

| 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Arg | Lys | Thr | Ser | Glu | Arg | Ser | Gln | Pro | Arg | Gly | Arg | Arg | Gln | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Pro | Lys | Ala | Arg | Arg | Pro | Glu | Gly | Arg | Ala | Trp | Ala | Gln | Pro | Gly |
|     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |
| Tyr | Pro | Trp | Pro | Leu | Tyr | Gly | Asn | Glu | Gly | Met | Gly | Trp | Ala | Gly | Trp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Leu | Ser | Pro | Arg | Gly | Ser | Arg | Pro | Ser | Trp | Gly | Pro | Thr | Asp | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Arg | Arg | Ser | Arg | Asn | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Phe | Ala | Asp | Leu | Val | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Gly | Ala | Ala | Arg | Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp |
|     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |
| Gly | Val | Asn | Tyr | Ala | Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Phe | Leu | Leu | Ala | Leu | Leu | Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser | Ala | Tyr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Val | Arg | Asn | Val | Ser | Gly | Met | Tyr | His | Val | Thr | Asn | Asp | Cys | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asn | Ser | Ser | Ile | Val | Tyr | Glu | Ala | Ala | Asp | Met | Ile | Met | His | Thr | Pro |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | Cys | Val | Pro | Cys | Val | Arg | Glu | Asn | Asn | Ser | Ser | Arg | Cys | Trp | Val |
|     | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |
| Ala | Leu | Thr | Pro | Thr | Leu | Ala | Ala | Arg | Asn | Ala | Ser | Val | Pro | Thr | Thr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Thr | Ile | Arg | Arg | His | Val | Asp | Leu | Leu | Val | Gly | Ala | Ala | Ala | Phe | Cys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Ala | Met | Tyr | Val | Gly | Asp | Leu | Cys | Gly | Ser | Val | Phe | Leu | Val | Ser |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gln | Leu | Phe | Thr | Ile | Ser | Pro | Arg | Arg | His | Glu | Thr | Val | Gln | Asp | Cys |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asn | Cys | Ser | Ile | Tyr | Pro | Gly | His | Ile | Thr | Gly | His | Arg | Met | Ala | Trp |
|     | 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |
| Asp | Met | Met | Met | Asn | Trp | Ser | Pro | Thr | Thr | Ala | Leu | Val | Val | Ser | Gln |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Leu | Leu | Arg | Ile | Pro | Gln | Ala | Val | Val | Asp | Met | Val | Ala | Gly | Ala | His |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Trp | Gly | Val | Leu | Ala | Gly | Leu | Ala | Tyr | Tyr | Ser | Met | Val | Gly | Asn | Trp |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ala | Lys | Val | Leu | Val | Val | Met | Leu | Leu | Phe | Ala | Gly | Val | Asp | Gly | His |

| 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Arg | Val | Ser | Gly | Gly | Ala | Ala | Ala | Ser | Asp | Thr | Arg | Gly | Leu | Val |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Ser | Leu | Phe | Ser | Pro | Gly | Ser | Ala | Gln | Lys | Ile | Gln | Leu | Val | Asn | Thr |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Asn | Gly | Ser | Trp | His | Ile | Asn | Arg | Thr | Ala | Leu | Asn | Cys | Asn | Asp | Ser |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Leu | Gln | Thr | Gly | Phe | Phe | Ala | Ala | Leu | Phe | Tyr | Lys | His | Lys | Phe | Asn |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Ser | Ser | Gly | Cys | Pro | Glu | Arg | Leu | Ala | Ser | Cys | Arg | Ser | Ile | Asp | Lys |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Phe | Ala | Gln | Gly | Trp | Gly | Pro | Leu | Thr | Tyr | Thr | Glu | Pro | Asn | Ser | Ser |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Asp | Gln | Arg | Pro | Tyr | Cys | Trp | His | Tyr | Ala | Pro | Arg | Pro | Cys | Gly | Ile |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Val | Pro | Ala | Ser | Gln | Val | Cys | Gly | Pro | Val | Tyr | Cys | Phe | Thr | Pro | Ser |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Pro | Val | Val | Val | Gly | Thr | Thr | Asp | Arg | Phe | Gly | Val | Pro | Thr | Tyr | Asn |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Trp | Gly | Ala | Asn | Asp | Ser | Asp | Val | Leu | Ile | Leu | Asn | Asn | Thr | Arg | Pro |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Pro | Arg | Gly | Asn | Trp | Phe | Gly | Cys | Thr | Trp | Met | Asn | Gly | Thr | Gly | Phe |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |
| Thr | Lys | Thr | Cys | Gly | Gly | Pro | Pro | Cys | Asn | Ile | Gly | Gly | Ala | Gly | Asn |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |
| Asn | Thr | Leu | Thr | Cys | Pro | Thr | Asp | Cys | Phe | Arg | Lys | His | Pro | Glu | Ala |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |
| Thr | Tyr | Ala | Arg | Cys | Gly | Ser | Gly | Pro | Trp | Leu | Thr | Pro | Arg | Cys | Met |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |
| Val | His | Tyr | Pro | Tyr | Arg | Leu | Trp | His | Tyr | Pro | Cys | Thr | Val | Asn | Phe |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |
| Thr | Ile | Phe | Lys | Val | Arg | Met | Tyr | Val | Gly | Gly | Val | Glu | His | Arg | Phe |
| 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |     |     |     | 640 |
| Glu | Ala | Ala | Cys | Asn | Trp | Thr | Arg | Gly | Glu | Arg | Cys | Asp | Leu | Glu | Asp |
|     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |
| Arg | Asp | Arg | Ser | Glu | Leu | Ser | Pro | Leu | Leu | Leu | Ser | Thr | Thr | Glu | Trp |
|     |     |     | 660 |     |     |     |     | 665 |     |     |     |     | 670 |     |     |
| Gln | Ile | Leu | Pro | Cys | Ser | Phe | Thr | Thr | Leu | Pro | Ala | Leu | Ser | Thr | Gly |
|     |     | 675 |     |     |     |     | 680 |     |     |     |     | 685 |     |     |     |
| Leu | Ile | His | Leu | His | Gln | Asn | Ile | Val | Asp | Val | Gln | Tyr | Leu | Tyr | Gly |
|     | 690 |     |     |     |     | 695 |     |     |     |     | 700 |     |     |     |     |

Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu  
 705 710 715 720  
 Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp  
 725 730 735  
 Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val  
 740 745 750  
 Val Leu Asn Ala Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe  
 755 760 765  
 Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro  
 770 775 780  
 Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu Leu  
 785 790 795 800  
 Leu Ala Leu Pro Pro Arg Ala Tyr Ala  
 805

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 1..17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Ser Asn Ser Ser Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys  
 1 5 10 15  
 Val

(2) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 1..22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Gly Gly Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
 1 5 10 15  
 Ser Pro Thr Thr Ala Leu  
 20

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 1..37

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys  
 1 5 10 15  
 Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr  
 20 25 30  
 Pro Gly Cys Gly Lys  
 35

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 1..25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Gly Gly Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr  
 1 5 10 15  
 Gln Leu Arg Arg His Ile Asp Leu Leu  
 20 25

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:





## (2) INFORMATION FOR SEQ ID NO: 58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```

Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala His Asp Ala Ile
1 5 10 15
Leu His Thr Pro
 20

```

## (2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```

Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr
1 5 10 15
Pro Gly Cys Val
 20

```

## (2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

```

His Asp Ala Ile Leu His Thr Pro Gly Val Pro Cys Val Arg Glu Gly
1 5 10 15
Asn Val Ser

```

## (2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

- Cys Val Arg Glu Gly Asn Val Ser Arg Cys Trp Val Ala Met Thr Pro  
1 5 10 15  
Thr Val Ala Thr  
20

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr  
1 5 10 15  
Gln Leu Arg Arg  
20

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear.

- (ii) MOLECULE TYPE: peptide

- Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser  
1 5 10 15  
Ala Thr Leu Cys  
20

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

|                 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu             | Val | Gly | Ser | Ala | Thr | Leu | Cys | Ser | Ala | Leu | Tyr | Val | Gly | Asp | Leu |
| 1               |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Cys Gly Ser Val |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 20              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

|                 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln             | Leu | Phe | Thr | Phe | Ser | Pro | Arg | Arg | His | Trp | Thr | Thr | Gln | Gly | Cys |
| 1               |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Asn Cys Ser Ile |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 20              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

|                 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr             | Gln | Gly | Cys | Asn | Cys | Ser | Ile | Tyr | Pro | Gly | His | Ile | Thr | Gly | His |
| 1               |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Arg Met Ala Trp |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 20              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

```

Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro
1 5 10 15

Thr Ala Ala Leu
 20

```

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

```

Asn Trp Ser Pro Thr Ala Ala Leu Val Met Ala Gln Leu Leu Arg Ile
1 5 10 15

Pro Gln Ala Ile
 20

```

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

```

Leu Leu Arg Ile Pro Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His
1 5 10 15

Trp Gly Val Leu
 20

```

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

Ala Gly Ala His Trp Gly Val Leu Ala Gly Ile Ala Tyr Phe Ser Met  
1 5 10 15  
Val Gly Asn Met  
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala Glu Thr Ile Val Ser  
1 5 10 15  
Gly Gly Gln Ala  
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

Ser Gly Leu Val Ser Leu Phe Thr Pro Gly Ala Lys Gln Asn Ile Gln  
1 5 10 15  
Leu Ile Asn Thr  
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

Gln Asn Ile Gln Leu Ile Asn Thr Asn Gly Gln Trp His Ile Asn Ser  
 1 5 10 15  
 Thr Ala Leu Asn  
 20

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

Leu Asn Cys Asn Glu Ser Leu Asn Thr Gly Trp Trp Leu Ala Gly Leu  
 1 5 10 15  
 Ile Tyr Gln His Lys  
 20

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

Ala Gly Leu Ile Tyr Gln His Lys Phe Asn Ser Ser Gly Cys Pro Glu  
 1 5 10 15  
 Arg Leu Ala Ser  
 20

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Pro Leu Thr Asp Phe Asp

1                      5                      10                      15  
 Gln Gly Trp Gly  
                     20

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

Thr Asp Phe Asp Gln Gly Trp Gly Pro Ile Ser Tyr Ala Asn Gly Ser  
 1                      5                      10                      15

Gly Pro Asp Gln  
                     20

(2) INFORMATION FOR SEQ ID NO: 78:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

Ala Asn Gly Ser Gly Pro Asp Gln Arg Pro Tyr Cys Trp His Tyr Pro  
 1                      5                      10                      15

Pro Lys Pro Cys  
                     20

(2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

Trp His Tyr Pro Pro Lys Pro Cys Gly Ile Val Pro Ala Lys Ser Val  
 1                      5                      10                      15

Cys Gly Pro Val

20

## (2) INFORMATION FOR SEQ ID NO: 80:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

|                 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala             | Lys | Ser | Val | Cys | Gly | Pro | Val | Tyr | Cys | Phe | Thr | Pro | Ser | Pro | Val |
| 1               |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val Val Gly Thr |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 20              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

|                 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro             | Ser | Pro | Val | Val | Val | Gly | Thr | Thr | Asp | Arg | Ser | Gly | Ala | Pro | Thr |
| 1               |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr Ser Trp Gly |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 20              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 82:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

|                 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly             | Ala | Pro | Thr | Tyr | Ser | Trp | Gly | Glu | Asn | Asp | Thr | Asp | Val | Phe | Val |
| 1               |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu Asn Asn Thr |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 20              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 83:



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

|                 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly             | Asn | Trp | Phe | Gly | Cys | Thr | Trp | Met | Asn | Ser | Thr | Gly | Phe | Thr | Lys |
| 1               |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val Cys Gly Ala |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 20              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 84:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

|                 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly             | Phe | Thr | Lys | Val | Cys | Gly | Ala | Pro | Pro | Val | Cys | Ile | Gly | Gly | Ala |
| 1               |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly Asn Asn Thr |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 20              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 85:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

|             |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile         | Gly | Gly | Ala | Gly | Asn | Asn | Thr | Leu | His | Cys | Pro | Thr | Asp | Cys | Arg |
| 1           |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys His Pro |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 86:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Thr Asp Cys Phe Arg Lys His Pro Asp Ala Thr Tyr Ser Arg Cys Gly  
 1 5 10 15

Ser Gly Pro Trp  
 20

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

Ser Arg Cys Gly Ser Gly Pro Trp Ile Thr Pro Arg Cys Leu Val Asp  
 1 5 10 15

Tyr Pro Tyr Arg  
 20

(2) INFORMATION FOR SEQ ID NO: 88:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Cys Leu Val Asp Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Ile  
 1 5 10 15

Asn Tyr Thr Ile  
 20

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

|                 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro             | Cys | Thr | Ile | Asn | Tyr | Thr | Ile | Phe | Lys | Ile | Arg | Met | Tyr | Val | Gly |
| 1               |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly Val Glu His |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 20              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 90:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

|                 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met             | Tyr | Val | Gly | Gly | Val | Glu | His | Arg | Leu | Glu | Ala | Ala | Cys | Asn | Trp |
| 1               |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr Pro Gly Glu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 20              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 91:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

|                 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala             | Cys | Asn | Trp | Thr | Pro | Gly | Glu | Arg | Cys | Asp | Leu | Glu | Asp | Arg | Asp |
| 1               |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg Ser Glu Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 20              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Thr Thr Thr  
 1 5 10 15  
 Gln Trp Gln Val  
 20

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

Tyr Gln Val Arg Asn Ser Thr Gly Leu  
 1 5

(2) INFORMATION FOR SEQ ID NO: 94:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

ACGTCCGTAC GTTCGAATTA ATTAATCGA

29

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 60 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

CCTCCGGACG TGCACTAGCT CCCGTCTGTG GTAGTGGTGG TAGTGATTAT CAATTAATTG

60

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

GTTTAACCAC TGCATGATG

19

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

GTCCCATCGA GTGCGGCTAC

20

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 45 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

CGTGACATGG TACATTCCGG ACACTTGGCG CACTTCATAA GCGGA

45

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

TGCCTCATAC ACAATGGAGC TCTGGGACGA GTCGTTCTGTG AC

42

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

TACCCAGCAG CGGGAGCTCT GTTGCTCCCG AACGCAGGGC AC

42

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

TGTCGTGGTG GGGACGGAGG CCTGCCTAGC TGCGAGCGTG GG

42

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

CGTTATGTGG CCCGGGTAGA TTGAGCACTG GCAGTCCTGC ACCGTCTC

48

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

CAGGGCCGTT CTAGGCCTCC ACTGCATCAT CATATCCCAA GC

42

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

CCGGAATGTA CCATGTCACG AACGAC

26

## (2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:  
GCTCCATTGT GTATGAGGCA GCGG

24

## (2) INFORMATION FOR SEQ ID NO: 106:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:  
GAGCTCCCGC TGCTGGGTAG CGC

23

## (2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:  
CCTCCGTCCC CACCACGACA ATACG

25

## (2) INFORMATION FOR SEQ ID NO: 108:



- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

CTACCCGGGC CACATAACGG GTCACCG

27

(2) INFORMATION FOR SEQ ID NO: 109:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

GGAGGCCTAC AACGGCCCTG GTGG

24

(2) INFORMATION FOR SEQ ID NO: 110:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

TTCTATCGAT TAAATAGAAT TC

22

(2) INFORMATION FOR SEQ ID NO: 111:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid

(ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
(iii) ANTI-SENSE: NO

23

## (2) INFORMATION FOR SEQ ID NO: 112:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys  
 1                      5                      10                      15  
 Ser Asn Ser Ser  
                     20

## (2) INFORMATION FOR SEQ ID NO: 113:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp  
 1                      5                      10                      15  
 Met Ile Met His Thr  
                     20

## (2) INFORMATION FOR SEQ ID NO: 114:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val  
 1                      5                      10                      15

Arg Glu Asn Asn Ser  
20

(2) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

Pro Cys Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu  
1 5 10 15

Thr Pro Thr Leu Ala  
20

(2) INFORMATION FOR SEQ ID NO: 116:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala Ser Val Pro  
1 5 10 15

Thr Thr Thr Ile Arg  
20

(2) INFORMATION FOR SEQ ID NO: 117:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

|                     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser                 | Val | Pro | Thr | Thr | Thr | Ile | Arg | Arg | His | Val | Asp | Leu | Leu | Val |
| 1                   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |
| Gly Ala Ala Ala Phe |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 20                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 118:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

|                     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu                 | Leu | Val | Gly | Ala | Ala | Ala | Phe | Cys | Ser | Ala | Met | Tyr | Val | Gly |
| 1                   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |
| Asp Leu Cys Gly Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 20                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 119:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

|                     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr                 | Val | Gly | Asp | Leu | Cys | Gly | Ser | Val | Phe | Leu | Val | Ser | Gln | Leu |
| 1                   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |
| Phe Thr Ile Ser Pro |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 20                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 120:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gln | Leu | Phe | Thr | Ile | Ser | Pro | Arg | Arg | His | Glu | Thr | Val | Gln |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |

|     |     |     |     |     |
|-----|-----|-----|-----|-----|
| Asp | Cys | Asn | Cys | Ser |
|     |     |     |     | 20  |

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Val | Gln | Asp | Cys | Asn | Cys | Ser | Ile | Tyr | Pro | Gly | His | Ile | Thr |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |

|     |     |     |     |     |
|-----|-----|-----|-----|-----|
| Gly | His | Arg | Met | Ala |
|     |     |     |     | 20  |

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Ile | Thr | Gly | His | Arg | Met | Ala | Trp | Asp | Met | Met | Met | Asn | Trp |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |

|     |     |     |     |     |
|-----|-----|-----|-----|-----|
| Ser | Pro | Thr | Thr | Ala |
|     |     |     |     | 20  |

*Cancelled*